



# **STIC Search Report**

## **Biotech-Chem Library**

STIC Database Tracking Number: 112348

To: Karen A Lacourciere

Location: REM-2D15

Art Unit: 1635

Wednesday, January 21, 2004

Case Serial Number: 09/423035

From: Beverly Shears

Location: Remsen Bldg.

RM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

### Search Notes

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STIC-Biotech/ChemLib

112348

From: Lacourciere, Karen  
Sent: Friday, January 16, 2004 2:13 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search 09/423,035

Please search SEQ ID NO:122 and 121 for 09/423,035 in the commercial databases. Please length limit the search to hits less than 100 nucleotides in length.

Thanks-  
Karen

*Karen A. Lacourciere Ph.D.*

Remsen 2D15 GAU 1635  
(571) 272-0759

CRFE

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
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# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 01-21-04  
Searcher: Beverly C 2528  
Terminal time: 33  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 38  
Number of Searches: \_\_\_\_\_  
Number of Databases: 2

### Search Site

\_\_\_\_\_ STIC  
\_\_\_\_\_ CM-1  
\_\_\_\_\_ Pre-S  
**Type of Search**  
\_\_\_\_\_ N.A. Sequence  
\_\_\_\_\_ A.A. Sequence  
\_\_\_\_\_ Structure  
\_\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_\_ IG  
☒ STN  
\_\_\_\_\_ Dialog  
\_\_\_\_\_ APS  
\_\_\_\_\_ Geninfo  
\_\_\_\_\_ SDC  
☒ DARC/Questel  
☒ Other CGN

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L1 FILE 'REGISTRY' ENTERED AT 12:29:20 ON 21 JAN 2004  
37479 S RGGCTAGC[HT]ACAACGA/SQSN

L7 37 S L1 AND SQL=<20

L8 FILE 'HCAPLUS' ENTERED AT 12:39:58 ON 21 JAN 2004  
26 S L7

L8 ANSWER 1 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2003:1007150 HCAPLUS  
TITLE: Antisense oligonucleotides against the PIM1 gene  
for use in analgesia  
INVENTOR(S): Altan, Oezlem; Kurreck, Jens; Gruenweller,  
Arnold; Erdmann, Volker  
PATENT ASSIGNEE(S): Gruenenthal G.m.b.H., Germany  
SOURCE: PCT Int. Appl., 37 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: German  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003106681	A2	20031224	WO 2003-EP6158	20030612
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: DE 2002-10226702 A 20020614  
AB Antisense DNA for use in inhibiting expression of the PIM1 gene are described for use in the diagnosis and control of PIM1 kinase-mediated pain perception. Use of PIM1 antisense oligonucleotides injected into the spinal cord to increase the threshold of pain perception is demonstrated in rat.  
IT 638223-95-7  
RL: PRP (Properties)  
(unclaimed nucleotide sequence; antisense oligonucleotides against the PIM1 gene for use in analgesia)

L8 ANSWER 2 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2003:971390 HCAPLUS  
DOCUMENT NUMBER: 140:26917  
TITLE: Antibodies having specificity for  
2'-deoxy-2'-C-allyl uridine-containing nucleic acids, and their use in detecting and monitoring therapeutic nucleic acid molecules in mammalian biological samples  
INVENTOR(S): Radka, Susan; Beigelman, Leonid; Peter, Haeberli  
PATENT ASSIGNEE(S): USA

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09/423035

SOURCE: U.S. Pat. Appl. Publ., 38 pp.  
 CODEN: USXXCO  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 1  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003228590	A1	20031211	US 2003-366191	20030212
PRIORITY APPLN. INFO.:			US 2002-356298P	P 20020213

AB The present invention relates to antibodies, antibody conjugates, and compns. thereof, methods of antibody synthesis, and applications of antibodies useful for the in vivo-detection of nucleic acid mols. containing 2'-deoxy-2'-C-allyl Uridine, such as in a clin. setting. The antibodies of the invention are also useful as screening agents which allow the selection of candidate therapeutic mols. for optimum bioavailability and/or activity, and as agents for cell and tissue specific-delivery of nucleic acid mols. The example discloses the development of a monoclonal antibody, CAIUSR, and its use for detection of the ANGIOZYME® ribozyme therapeutic in vivo. This antibody was developed for use in monitoring clin. trials of ANGIOZYME.

IT 633370-08-8

RL: PRP (Properties)  
 (unclaimed nucleotide sequence; antibodies having specificity for 2'-deoxy-2'-C-allyl uridine-containing nucleic acids, and their use in detecting and monitoring therapeutic nucleic acid mols. in mammalian biol. samples)

L8 ANSWER 3 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:855650 HCAPLUS  
 DOCUMENT NUMBER: 139:317479  
 TITLE: Nucleic acid-based modulation of NOGO and NOGO receptor interactions and genes for treatment and/or diagnosis of associated diseases  
 INVENTOR(S): Blatt, Lawrence; McSwiggen, James; Chowrira, Bharat M.; Haeberli, Peter  
 PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA  
 SOURCE: U.S. Pat. Appl. Publ., 77 pp., Cont.-in-part of Appl. No. PCT/US02/10512.  
 CODEN: USXXCO  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 12  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003203870	A1	20031030	US 2003-430882	20030506
WO 2001059103	A2	20010816	WO 2001-US4273	20010209
WO 2001059103	A3	20020613		
WO 2001059103	C2	20021024		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,

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UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,  
TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,  
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,  
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,  
TG  
US 2003060611 A1 20030327 US 2001-780533 20010209  
US 2003113891 A1 20030619 US 2001-827395 20010405  
WO 2002081628 A2 20021017 WO 2002-US10512 20020403  
WO 2002081628 A3 20030220  
WO 2002081628 C1 20030828  
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
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GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,  
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,  
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM,  
AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,  
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,  
SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,  
SN, TD, TG  
PRIORITY APPLN. INFO.:  
US 2000-181797P P 20000211  
US 2001-780533 B2 20010209  
WO 2001-US4273 A2 20010209  
US 2001-827395 B1 20010405  
WO 2002-US10512 A2 20020403  
US 2000-185516P P 20000228  
US 2000-187128P P 20000306  
US 2001-294412P P 20010529  
US 2001-315315P P 20010828  
AB The present invention relates to nucleic acid mols., including  
aptamers and antisense and enzymic nucleic acid mols., such as  
hammerhead ribozymes, DNazymes, and antisense oligonucleotides,  
which modulate the expression of NOGO and NOGO receptor genes. In  
particular, novel nucleic acid-based techniques are provided to  
inhibit the expression of NOGO-A, NOGO-B, and/or NOGO-C, NOGO-66  
receptor, and/or NI-250, myelin-associated glycoprotein, tenascin-R,  
and NG-2. The sequence of human NOGO and NOGO receptor genes are  
screened for accessible sites using a computer-folding algorithm;  
regions of the RNA that do not form secondary folding structures and  
contain potential enzymic nucleic acid mol and/or antisense  
binding/cleaving sites are identified. The nucleic acids of the  
present invention can be used to treat a patient having a condition  
associated with the level of NOGO or NOGO receptor.  
IT 613321-58-7  
RL: PRP (Properties)  
(unclaimed nucleotide sequence; nucleic acid-based modulation of  
NOGO and NOGO receptor interactions and genes for treatment  
and/or diagnosis of associated diseases)  
L8 ANSWER 4 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2003:731500 HCAPLUS  
DOCUMENT NUMBER: 139:224402  
TITLE: Enzymatic nucleic acid treatment of diseases or  
conditions related to hepatitis C virus  
infection  
INVENTOR(S): Blatt, Lawrence; McSwiggen, James; Roberts,

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PATENT ASSIGNEE(S): Elisabeth; Pavco, Pamela A.; MacJack, Dennis  
SOURCE: USA  
U.S. Pat. Appl. Publ., 172 pp., Cont.-in-part of  
U.S. Ser. No. 740,332.  
CODEN: USXXCO  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 104  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003171311	A1	20030911	US 2001-817879	20010326
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
US 2002082225	A1	20020627	US 1999-274553	19990323
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 2002013458	A1	20020131	US 2000-504231	20000215
US 2003125270	A1	20030703	US 2000-740332	20001218
PRIORITY APPLN. INFO.:			US 1998-83217P	P 19980427
			US 1998-100842P	P 19980918
			US 1999-257608	B2 19990225
			US 1999-274553	A2 19990323
			US 2000-504231	A2 20000215
			US 2000-611931	A2 20000707
			US 2000-740332	A2 20001218
			AU 1995-26422	A3 19950518
			US 1996-623891	A 19960325

AB This invention relates to enzymic nucleic acid mols. (e.g., ribozymes and DNazymes) directed to cleave RNA species of hepatitis C virus (HCV) and/or encoded by the HCV. Specifically, the present invention describes enzymic nucleic acid mols. that would cleave in the conserved regions of the HCV genome. In a preferred embodiment, the invention features the use of an enzymic nucleic acid mol., preferably in the hammerhead, Inozyme (NCH), G-cleaver, Amberzyme, Zinzyme and/or DNazyme motif, to inhibit the expression and/or replication of HCV. Chemical modifications in the sugar, base, and/or phosphate backbones of these enzymic nucleic acids is carried out to improve their stability. Such enzymic nucleic acid mols. may be used to treat diseases associated with HCV infection. Ribozymes in combination with interferons and polyethylene glycol interferons which have the potential to improve the effectiveness of treatment of HCV are also described. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 591261-44-8

RL: PRP (Properties)

(unclaimed nucleotide sequence; enzymic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection)

L8 ANSWER 5 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:568525 HCAPLUS

DOCUMENT NUMBER: 139:358722

TITLE: Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection

INVENTOR(S): Blatt, Lawrence; McSwiggen, James; Roberts,

Searcher : Shears 571-272-2528

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PATENT ASSIGNEE(S): Elisabeth; Pavco, Pamela A.; Macejack, Dennis  
SOURCE: USA  
U.S. Pat. Appl. Publ., 198 pp.  
CODEN: USXXCO  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 104  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003125270	A1	20030703	US 2000-740332	20001218
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 2003125270	A1	20030703	US 2000-740332	20001218
PRIORITY APPLN. INFO.:			US 2000-740332	A 20001218
			AU 1995-26422	A3 19950518
			US 1996-623891	A 19960325

AB This invention relates to enzymic nucleic acid mols. (e.g., ribozymes and DNazymes) directed to cleave RNA species of hepatitis C virus (HCV) and/or encoded by the HCV. Specifically, the present invention describes enzymic nucleic acid mols. that would cleave in the conserved regions of the HCV genome. In a preferred embodiment, the invention features the use of an enzymic nucleic acid mol., preferably in the hammerhead, Inozyme (NCH), G-cleaver, amberzyme, zinzyme and/or DNazyme motif, to inhibit the expression and/or replication of HCV. Chemical modifications in the sugar, base, and/or phosphate backbones of these enzymic nucleic acids is carried out to improve their stability. Such enzymic nucleic acid mols. may be used to treat diseases associated with HCV infection. Ribozymes in combination with interferons and polyethylene glycol interferons which have the potential to improve the effectiveness of treatment of HCV are also described. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 557143-59-6  
RL: PRP (Properties)  
(unclaimed nucleotide sequence; enzymic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection)

L8 ANSWER 6 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2003:309404 HCAPLUS  
DOCUMENT NUMBER: 139:143909  
TITLE: Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors  
INVENTOR(S): Akhtar, Saghir; McSwiggen, James  
PATENT ASSIGNEE(S): Kuwait  
SOURCE: U.S. Pat. Appl. Publ., 199 pp., Cont.-in-part of U.S. Ser. No. 401,063.  
CODEN: USXXCO  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 104  
PATENT INFORMATION:

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PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003073207	A1	20030417	US 2001-848754	20010503
US 6057156	A	20000502	US 1997-985162	19971204
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 6623962	B1	20030923	US 1999-401063	19990922
PRIORITY APPLN. INFO.:			US 1997-36476P P	19970131
			US 1997-985162 A1	19971204
			US 1999-401063 A2	19990922
			AU 1995-26422 A3	19950518
			US 1996-623891 A	19960325

AB The present invention relates to nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, allozymes and antisense, which modulate the expression of epidermal growth factor receptor genes. The sequence of human epidermal growth factor receptor (EGFR) gene is screened for accessible sites using a computer-folding algorithm. Regions of the RNA that do not form secondary folding structures and contain potential enzymic nucleic acid mol. and/or antisense binding/cleavage sites are identified and used to design the complementary regions of the antisense and enzymic nucleic acid mols. Two human cell lines, A549 lung carcinoma cells and SKOV3 ovarian carcinoma cells known to express medium to high levels of EGFR protein, are used in anti-proliferation assays for nucleic acid screening. The invention designs, synthesizes and tests nucleic acid mols. that target both EGFR and HER2 RNA in cell proliferation and RNA reduction assays for potential use in treating cancer. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 506617-43-2

RL: PRP (Properties)

(unclaimed nucleotide sequence; enzymic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors)

L8 ANSWER 7 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:261042 HCAPLUS

DOCUMENT NUMBER: 138:282290

TITLE: Methods and kits containing nucleic acid-based enzymes for detection of single nucleotide polymorphisms in diagnosis of diseases

INVENTOR(S): Usman, Nassim; McSwiggen, James A.; Zinnen, Shawn; Seiwert, Scott; Haeberli, Peter; Chowrira, Bharat; Blatt, Lawrence; Vaish, Narendra K.

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 116 pp., Cont.-in-part of U.S. Ser. No. 992,160.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 12

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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US 2003065155 A1 20030403 US 2002-56761 20020123  
WO 2001066721 A2 20010913 WO 2001-US7163 20010306  
WO 2001066721 A3 20020725  
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GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
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US 2002102568 A1 20020801 US 2001-877526 20010608  
US 2003008295 A1 20030109 US 2001-992160 20011105  
WO 2003089650 A2 20031030 WO 2002-US35529 20021105  
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US 2004009510 A1 20040115 US 2003-422050 20030423  
PRIORITY APPLN. INFO.: US 2000-187128P P 20000306  
US 2001-800594 A2 20010306  
WO 2001-US7163 W 20010306  
US 2001-877526 A2 20010608  
US 2001-992160 A2 20011105  
US 2002-56761 A 20020123  
US 2002-283858 A 20021030  
US 2002-286492 A 20021101  
WO 2002-US35529 A2 20021105  
AB Nucleic acid sensor mols. and methods are provided for the detection  
and amplification of signaling agents using enzymic nucleic acid  
constructs, including hammerhead enzymic nucleic acid mols.,  
inozymes, G-cleaver enzymic nucleic acid mols., zinzymes, amberzymes  
and DNazymes. Also provided are kits for detection and  
amplification. The nucleic acid sensor mols., methods and kits  
provided herein can be used in diagnostics, nucleic acid circuits,  
nucleic acid computers, therapeutics, target validation, target  
discovery, drug optimization, single nucleotide polymorphism (SNP)  
detection, single nucleotide polymorphism (SNP) scoring, and  
proteome scoring as well as other uses described herein.  
IT 504513-55-7  
RL: PRP (Properties)  
(unclaimed nucleotide sequence; methods and kits containing nucleic  
acid-based enzymes for detection of single nucleotide  
polymorphisms in diagnosis of diseases)  
L8 ANSWER 8 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2003:261013 HCAPLUS

Searcher : Shears 571-272-2528

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09/423035

DOCUMENT NUMBER: 138:292713  
 TITLE: Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors  
 INVENTOR(S): Akhtar, Saghir; McSwiggen, James  
 PATENT ASSIGNEE(S): Kuwait  
 SOURCE: U.S. Pat. Appl. Publ., 113 pp., Cont.-in-part of U.S. Ser. No. 848,754.  
 CODEN: USXXCO  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 104  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003064945	A1	20030403	US 2001-916466	20010725
US 6057156	A	20000502	US 1997-985162	19971204
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 6623962	B1	20030923	US 1999-401063	19990922
US 2003073207	A1	20030417	US 2001-848754	20010503
US 2003170891	A1	20030911	US 2002-251117	20020919
US 2003186909	A1	20031002	US 2002-277494	20021021
WO 2003070912	A2	20030828	WO 2003-US5045	20030220
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:

US 1997-36476P	P	19970131
US 1997-985162	A1	19971204
US 1999-401063	A2	19990922
US 2001-848754	A2	20010503
AU 1995-26422	A3	19950518
US 1996-623891	A	19960325
US 1997-36749P	P	19970127
US 2001-296249P	P	20010606
US 2001-916466	A2	20010725
US 2002-358580P	P	20020220
US 2002-363124P	P	20020311
WO 2002-US16840	A1	20020529
US 2002-163552	A2	20020606
US 2002-386782P	P	20020606
US 2002-393924P	P	20020703
US 2002-406784P	P	20020829
US 2002-408378P	P	20020905
US 2002-409293P	P	20020909
US 2002-251117	A1	20020919
US 2002-277494	A1	20021021
US 2003-440129P	P	20030115

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AB The present invention relates to nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, allozymes and antisense, which modulate the expression of epidermal growth factor receptor genes.

IT 503875-66-9  
RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
(enzymic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors)

L8 ANSWER 9 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2003:76966 HCAPLUS  
DOCUMENT NUMBER: 138:142441  
TITLE: Enzymatic nucleic acid peptide conjugates  
INVENTOR(S): Beigelman, Leonid; Azhayev, Alex; Azhayeva, Elena  
PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA; Antopolsky, Maxim  
SOURCE: PCT Int. Appl., 88 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008628	A2	20030130	WO 2002-US23324	20020722
WO 2003008628	A3	20031030		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003148928	A1	20030807	US 2002-201389	20020722
PRIORITY APPLN. INFO.:			US 2001-306995P	P 20010720
OTHER SOURCE(S):	MARPAT 138:142441			

AB This invention features conjugates, compns., methods of synthesis, and applications thereof, including galactose, galactosamine, N-acetyl galactosamine, PEG, phospholipid, and human serum albumin (HSA) derived conjugates of nucleosides, nucleotides, non-nucleosides, and nucleic acids including enzymic nucleic acids, DNazymes, allozymes, antisense, dsRNA, siRNA, triplex oligonucleotides, 2,5-A chimeras, decoys and aptamers.

IT 493068-33-0  
RL: PRP (Properties)  
(unclaimed nucleotide sequence; enzymic nucleic acid peptide conjugates)

L8 ANSWER 10 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2003:23421 HCAPLUS  
DOCUMENT NUMBER: 138:84437

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09/423035

TITLE: Methods and kits containing nucleic acid-based enzymes for detection of single nucleotide polymorphisms in diagnosis of diseases  
 INVENTOR(S): Usman, Nassim; McSwiggen, James A.; Zinnen, Shawn; Seiwert, Scott; Haeberli, Peter; Chowrira, Bharat; Blatt, Lawrence; Vaish, Narendra  
 PATENT ASSIGNEE(S): USA  
 SOURCE: U.S. Pat. Appl. Publ., 100 pp., Cont.-in-part of U.S. Pat. Appl. 2002 102,568.  
 CODEN: USXXCO  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 12  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003008295	A1	20030109	US 2001-992160	20011105
WO 2001066721	A2	20010913	WO 2001-US7163	20010306
WO 2001066721	A3	20020725		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 2002102568	A1	20020801	US 2001-877526	20010608
US 2003065155	A1	20030403	US 2002-56761	20020123
WO 2003089650	A2	20031030	WO 2002-US35529	20021105
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004009510	A1	20040115	US 2003-422050	20030423
PRIORITY APPLN. INFO.:				
			US 2000-187128P	P 20000306
			US 2001-800594	A2 20010306
			WO 2001-US7163	W 20010306
			US 2001-877526	A2 20010608
			US 2001-992160	A2 20011105
			US 2002-56761	A 20020123
			US 2002-283858	A 20021030
			US 2002-286492	A 20021101
			WO 2002-US35529	A2 20021105

AB The present invention provides nucleic acid sensor mols. and methods for the detection and amplification of signaling agents using

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enzymic nucleic acid constructs. These include hammerhead enzymic nucleic acid mols., inozymes, G-cleaver enzymic nucleic acid mols., zinzymes, amberzymes and DNAzymes. Kits for detection and amplification and uses of the invention in diagnostics, nucleic acid circuits, nucleic acid computers, therapeutics, target validation, target discovery, drug optimization, SNP detection, SNP scoring, proteome scoring and other uses are disclosed.

IT 483392-16-1

RL: PRP (Properties)

(unclaimed nucleotide sequence; methods and kits containing nucleic acid-based enzymes for detection of single nucleotide polymorphisms in diagnosis of diseases)

L8 ANSWER 11 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:974509 HCAPLUS

DOCUMENT NUMBER: 139:46323

TITLE: Cellular uptake, distribution, and stability of 10 - 23 deoxyribozymes

AUTHOR(S): Dass, Crispin R.; Saravolac, Edward G.; Li, Yang; Sun, Lun-Quan

CORPORATE SOURCE: Johnson and Johnson Research Laboratories, Eveleigh, 1430, Australia

SOURCE: Antisense & Nucleic Acid Drug Development (2002), 12(5), 289-299  
CODEN: ANADF5; ISSN: 1087-2906

PUBLISHER: Mary Ann Liebert, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The cellular uptake, intracellular distribution, and stability of 33-mer deoxyribozyme oligonucleotides (DNAzymes) were examined in several cell lines. PAGE anal. revealed that there was a weak association between the DNAzyme and DOTAP or Superfect transfection reagents at charge ratios that were minimally toxic to cultured cells. Cellular uptake was analyzed by cell fractionation of radiolabeled DNAzyme, by FACS, and by fluorescent microscopic anal. of FITC-labeled and TAMRA-labeled DNAzyme. Altering DNAzyme size and chemical did not significantly affect uptake into cells. Inspection of paraformaldehyde-fixed cells by fluorescence microscopy revealed that DNAzyme was distributed primarily in punctate structures surrounding the nucleus and that substantial delivery to the nucleus was not observed up to 24 h after initiation of transfection. Incubation in human serum or plasma demonstrated that a 3'-inversion modification greatly increased DNAzyme stability ( $t_{1/2} \approx 22$  h) in comparison to the unmodified form ( $t_{1/2} \approx 70$  min). The 3'-inversion-modified DNAzymes remained stable during cellular uptake, and catalytically active oligonucleotide could be extracted from the cells 24 h posttransfection. In smooth muscle cell proliferation assay, the modified DNAzyme targeting the c-myc gene showed a much stronger inhibitory effect than did the unmodified version. The present study demonstrates that DNAzymes with a 3'-inversion are readily delivered into cultured cells and are functionally stable for several hours in serum and within cells.

IT 543745-67-1D, 5'-FITC labeled

RL: PAC (Pharmacological activity); PKT (Pharmacokinetics); THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
(cellular uptake, distribution, and stability of 10-23 deoxyribozymes)

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REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L8 ANSWER 12 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2002:927617 HCAPLUS  
DOCUMENT NUMBER: 138:19530  
TITLE: Nucleic acid treatment of diseases or conditions  
related to levels of Ras, HER2 and HIV  
INVENTOR(S): McSwiggen, James  
PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Incorporated, USA  
SOURCE: PCT Int. Appl., 185 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 104  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002097114	A2	20021205	WO 2002-US16840	20020529
WO 2002097114	A3	20030508		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
WO 2002097114	A2	20021205	WO 2002-XA16840	20020529
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003153521	A1	20030814	US 2002-238700	20020910
WO 2003070912	A2	20030828	WO 2003-US5045	20030220
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,			

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BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT,  
LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA,  
GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:

US 2001-294140P P 20010529  
US 2001-296249P P 20010606  
US 2001-318471P P 20010910  
AU 1995-26422 A3 19950518  
US 1996-623891 A 19960325  
US 2001-916466 A 20010725  
US 2002-358580P P 20020220  
US 2002-363124P P 20020311  
WO 2002-US16840 A 20020529  
US 2002-163552 A1 20020606  
US 2002-386782P P 20020606  
US 2002-393924P P 20020703  
US 2002-406784P P 20020829  
US 2002-408378P P 20020905  
US 2002-409293P P 20020909  
US 2002-251117 A1 20020919  
US 2002-277494 A1 20021021  
US 2003-440129P P 20030115

AB The present invention relates to nucleic acid mols., including enzymic nucleic acid mols., such as DNazymes (e.g. DNA enzymes, catalytic DNA), siRNA, aptamers, and antisense that modulate the expression of Ras genes such as K-Ras, H-Ras, and/or N-Ras, HIV genes such as HIV-1, and HER2 (c-erbB2) gene. The sequence of human HER2 or Ras genes were screened for accessible sites using a computer-folding algorithm. Regions of the RNA that do not form secondary folding structure and contain potential enzymic nucleic acid mol. and/or antisense binding/cleavage sites are identified. The sequences of c-Ki-ras, c-Ha-ras, HER2, and HIV RNA binding/cleavage sites are provided, as are the sequences of designed enzymic nucleic acid mols., e.g., hammerhead ribozymes, DNazymes, inozymes, zinzymes, and Amberzymes. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.]

IT 478129-01-0

RL: PRP (Properties)

(unclaimed nucleotide sequence; nucleic acid treatment of diseases or conditions related to levels of Ras, HER2 and HIV)

L8 ANSWER 13 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:828621 HCAPLUS

DOCUMENT NUMBER: 138:314544

TITLE: Oligonucleotide-mediated inhibition of hepatitis B virus and hepatitis C virus replication

INVENTOR(S): Blatt, Lawrence; Macejak, Dennis; McSwiggen, James; Morrissey, David; Pavco, Pamela; Lee, Patrice; Draper, Kenneth; Roberts, Elisabeth

PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA

SOURCE: PCT Int. Appl., 387 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 104

PATENT INFORMATION:

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09/423035

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 2002081494	A1	20021017	WO 2002-XD9187	20020326
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, ML, MR, NE, SN, TD, TG			
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 2003171311	A1	20030911	US 2001-817879	20010326
US 2003068301	A1	20030410	US 2001-877478	20010608
US 2003148985	A1	20030807	US 2002-310294	20021205
PRIORITY APPLN. INFO.:			US 2001-817879	A 20010326
			US 2001-296876P	P 20010608
			US 2001-877478	A 20010608
			US 2001-335059P	P 20011024
			US 2001-337055P	P 20011205
			US 1992-882712	B1 19920514
			US 1994-193627	A1 19940207
			AU 1995-26422	A3 19950518
			US 1996-623891	A 19960325
			US 1998-83217P	P 19980427
			US 1998-100842P	P 19980918
			US 1999-257608	B2 19990225
			US 1999-274553	A2 19990323
			US 1999-436430	A2 19991108
			US 2000-504231	A2 20000215
			US 2000-531025	A2 20000320
			US 2000-611931	A2 20000707
			US 2000-636385	A2 20000809
			US 2000-696347	A2 20001024
			US 2000-740332	A2 20001218
AB	The present invention relates to nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNAzymes, Inozymes, Zinzymes, Amberzymes, and G-cleaver ribozymes, which modulate the synthesis, expression and/or stability of a hepatitis C virus (HCV) or hepatitis B virus (HBV) RNA and methods for their use alone or in combination with other therapies. In addition, nucleic acid decoy mols. and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences and methods for their use alone or in combination with other therapies, are disclosed. Oligonucleotides that specifically bind the Enhancer I region of HBV DNA are further disclosed. The present invention further relates to the use of nucleic acids, such as decoy and aptamer mols. of the invention, to modulate the expression of HBV genes and HBV viral replication. Furthermore, HBV animal models and methods of use are disclosed, including methods of screening for compds. and/or potential therapies directed against HBV. The present invention also relates to compds., including enzymic nucleic acid mols., ribozymes, DNAzymes, nuclease-activating			

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comps. and chimeras such as 2',5'-adenylates, that modulate the expression and/or replication of HCV. [This abstract record is one of five records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 491672-93-6

RL: PRP (Properties)

(unclaimed nucleotide sequence; oligonucleotide-mediated inhibition of hepatitis B virus and hepatitis C virus replication)

L8 ANSWER 14 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:822462 HCAPLUS

DOCUMENT NUMBER: 138:265678

TITLE: Modulation of gene expression associated with inflammation, proliferation and neurite outgrowth using antisense and enzymic nucleic acid-based technologies

INVENTOR(S): Blatt, Lawrence; Chowrira, Bharat; Haeberli, Peter; McSwiggen, James; Fosnaugh, Kathy

PATENT ASSIGNEE(S): Ribozyne Pharmaceuticals, Incorporated, USA

SOURCE: PCT Int. Appl., 317 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 12

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002081628	A2	20021017	WO 2002-XC10512	20020403
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003113891	A1	20030619	US 2001-827395	20010405
US 2003119017	A1	20030626	US 2002-156306	20020528
US 2003143732	A1	20030731	US 2002-224005	20020820
US 2003148507	A1	20030807	US 2002-226992	20020823
US 2003191077	A1	20031009	US 2002-230006	20020828
PRIORITY APPLN. INFO.:			US 2001-827395	A 20010405
			US 2001-294412P	P 20010529
			US 2001-315315P	P 20010828
			US 2000-181797P	P 20000211
			US 2001-780533	A2 20010209

AB The present invention relates to nucleic acid mols., including antisense, enzymic nucleic acid mols., and RNA interference mols., which modulate the expression of genes encoding prostaglandin D2 receptor, adenosine receptor A1, NOGO receptor, I $\kappa$ B protein kinase, and protein kinase PKR. Thus, nucleic acids encoding these products are scanned to identify targets for cleavage by designed

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enzymic nucleic acids, such as hammerhead ribozymes, Inozymes, Zinzymes, DNAzymes, and Amberzymes. Chemical modifications in the sugar, base, and/or phosphate backbones of these enzymic nucleic acids is carried out to improve their stability. Inhibition of gene product expression may be used for treatment of diseases associated with said expression. [This abstract record is one of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 484802-52-0

RL: PRP (Properties)

(unclaimed nucleotide sequence; modulation of gene expression associated with inflammation, proliferation and neurite outgrowth using antisense and enzymic nucleic acid-based technologies)

L8 ANSWER 15 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:698624 HCAPLUS

DOCUMENT NUMBER: 138:66656

TITLE: Nucleic acid-based treatment of diseases or conditions related to West Nile virus infection

INVENTOR(S): Blatt, Lawrence; McSwiggen, James A.

PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA

SOURCE: PCT Int. Appl., 495 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 9

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002068637	A2	20020906	WO 2001-XH48350	20011019
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2002068637	A2	20020906	WO 2001-US48350	20011019
WO 2002068637	C1	20030515		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.:

US 2000-242411P P 20001020

WO 2001-US48350 A 20011019

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AB The present invention relates to nucleic acid mols. (e.g., ribozymes, DNAzymes, antisense oligonucleotides, triplex-forming oligonucleotides, 2-5A oligonucleotides, decoys) that modulate the expression and/or replication of West Nile Virus (WNV). Such enzymic and antisense nucleic acids can be used to diagnose and treat diseases associated with WNV infection, such as pancreatitis, encephalitis, myocarditis, meningitis, neurol. infection, hepatitis, liver failure, hepatocellular carcinoma, and cirrhosis. Thus, the sequence of human WNV was screened for accessible sites using a computer-folding algorithm; regions of the RNA that do not form secondary folding structures and contain potential enzymic nucleic acid and/or antisense binding/cleavage sites were identified. Enzymic nucleic acids mols. are designed that could bind each target and are individually analyzed by computer folding. Varying binding arm lengths can be chosen to optimize activity. Five different enzymic nucleic acid mols. of different motifs (hammerhead, inozyme, DNAzyme, Amberzyme, and zinzyme) show cleavage data with full-length or partially full-length, internally-labeled target RNA. The enzymic nucleic acid mols. are effective against WNV RNA in vivo (HeLa cells) and in animal models (mice infected with WNV). [This abstract record is one of nine records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 479786-61-3

RL: PRP (Properties)

(unclaimed nucleotide sequence; nucleic acid-based treatment of diseases or conditions related to West Nile virus infection)

L8 ANSWER 16 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:414955 HCAPLUS

DOCUMENT NUMBER: 137:121425

TITLE: A general strategy for effector-mediated control of RNA-cleaving ribozymes and DNA enzymes

AUTHOR(S): Wang, Dennis Y.; Lai, Beatrice H. Y.; Sen, Dipankar

CORPORATE SOURCE: Department of Molecular Biology & Biochemistry, Simon Fraser University, Burnaby, BC, V5A 1S6, Can.

SOURCE: Journal of Molecular Biology (2002), 318(1), 33-43

CODEN: JMOBAK; ISSN: 0022-2836

PUBLISHER: Elsevier Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A novel and general approach is described for generating versions of RNA-cleaving ribozymes (RNA enzymes) and DNAzymes (DNA enzymes), whose catalytic activity can be controlled by the binding of activator mols. Variants of the RNA-cleaving 10-23 DNAzyme and 8-17 DNAzyme were created, whose catalysis was activated by up to .apprx.35-fold by the binding of the effector adenosine. The design of such variants was possible even though the tertiary folding of the two DNAzymes is not known. Variants of the hammerhead ribozyme were constructed, to respond to the effectors ATP and FMN. Whereas in conventional allosteric ribozymes, effector-binding modulates the chemical step of catalysis, here, effectors exercise their effect upon the substrate-binding step, by stabilizing the enzyme-substrate complex. Because such an approach for controlling the activity of DNAzymes/ribozymes requires no prior knowledge of the enzyme's

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secondary or tertiary folding, this regulatory strategy should be generally applicable to any RNA-cleaving ribozyme or DNzyme, natural or in vitro selected, provided substrate-recognition is achieved by Watson-Crick base-pairing.

IT 444035-98-7

RL: BSU (Biological study, unclassified); CAT (Catalyst use); PRP (Properties); BIOL (Biological study); USES (Uses)

(DNzyme; design and properties of effector-mediated aptamer-containing DNzymes)

REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 17 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:171921 HCAPLUS

DOCUMENT NUMBER: 136:241681

TITLE: Antisense oligonucleotides against vanilloid receptor 1 (VR1), therapeutic and diagnostic uses, and screening method

INVENTOR(S): Kurreck, Jens; Erdmann, Volker A.

PATENT ASSIGNEE(S): Grunenthal GmbH, Germany

SOURCE: PCT Int. Appl., 76 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002018407	A2	20020307	WO 2001-EP10081	20010831
WO 2002018407	A3	20021003		
WO 2002018407	C2	20030515		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
DE 10043674	A1	20020321	DE 2000-10043674	20000902
DE 10043702	A1	20020314	DE 2000-10043702	20000904
AU 2001095531	A5	20020313	AU 2001-95531	20010831
EP 1313768	A2	20030528	EP 2001-976176	20010831
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
US 2004002473	A1	20040101	US 2003-376341	20030303
PRIORITY APPLN. INFO.:			DE 2000-10043674 A	20000902
			DE 2000-10043702 A	20000904
			WO 2001-EP10081 W	20010831

AB The invention provides antisense oligodeoxynucleotides against VR1, corresponding nucleotide constructs, cells containing the nucleotide constructs, pharmaceuticals and diagnostic substances, the use thereof in pain therapy, and methods for diagnosing symptoms related

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to VR1 and identifying pain-modulating substances.

IT 403777-66-2  
RL: PRP (Properties)  
(Unclaimed; antisense oligonucleotides against vanilloid receptor 1 (VR1), therapeutic and diagnostic uses, and screening method)

L8 ANSWER 18 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2002:122738 HCAPLUS  
DOCUMENT NUMBER: 136:194272  
TITLE: Ribozymes and antisense oligonucleotides for the inhibition of gene expression by calcium-activated chloride channel-1 gene CLCA-1  
INVENTOR(S): Thompson, James; McSwiggen, James; McKenzie, Timothy; Ayers, David; Szymkowski, David E.; Grupe, Andrew  
PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Incorporated, USA; Syntex (U.S.A.) LLC  
SOURCE: PCT Int. Appl., 152 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002011674	A2	20020214	WO 2001-US24970	20010809
WO 2002011674	A3	20030925		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003064946	A1	20030403	US 2001-927046	20010809
PRIORITY APPLN. INFO.:			US 2000-224383P P	20000809
AB	Nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, and GeneBlocs, which modulate the expression of calcium-activated chloride channels (CLCA1, CLCA2, CLCA3, and CLCA4) are provided. A target discovery target validation approach was used for finding genes that are involved in chronic mucous hypersecretion. The reporter system consists of a plasmid construct, termed pMUC5AC-EGFP, bearing a gene coding for green fluorescent protein (GFP). The promoter region of the GFP gene is replaced by a portion of the mucin 5AC promoter sufficient to direct efficient transcription of the GFP gene; the plasmid also contains the neomycin drug resistance gene. The cell line selected as host for these studies, NCI-H292 (ATCC CRL-1848), is derived from a human lung mucoepidermoid carcinoma. A ribozyme library with two randomized regions comprising six-nucleotide binding "arms" is used to enrich cells for non-responders to mucin induction and a bioinformatics approach used to identify human CLCA1 as a regulator of MUC5AC expression. Antisense, hammerhead,			

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DNAzyme, NCH, amberzyme, zinzyme, and G-Cleaver ribosome binding/cleavage sites in CLCA1 were identified. The nucleic acid mols. are individually analyzed by computer folding to assess whether the sequences fold into the appropriate secondary structure and to anneal to various sites in the RNA target. Those nucleic acid mols. with unfavorable intramol. interactions such as between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity.

IT 400185-65-1

RL: PRP (Properties)

(unclaimed nucleotide sequence; ribozymes and antisense oligonucleotides for the inhibition of gene expression by calcium-activated chloride channel-1 gene CLCA-1)

L8 ANSWER 19 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:582042 HCAPLUS

DOCUMENT NUMBER: 135:175355

TITLE: Nucleic acid reagents for inhibition of checkpoint kinase-1 gene expression for therapeutic use

INVENTOR(S): Fattaey, Ali R.; Jarvis, Thale; McSwiggen, James; Booher, Robert N.; Holman, Patricia S.

PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA

SOURCE: PCT Int. Appl., 115 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001057206	A2	20010809	WO 2001-US3504	20010202
WO 2001057206	A3	20020829		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

US 2003087847 A1 20030508 US 2001-776474 20010202

PRIORITY APPLN. INFO.: US 2000-179983P P 20000203

AB The present invention relates to nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNAzymes, and antisense, which modulate the expression of the Chk-1 gene. Inhibition of the enzyme may be useful in the treatment of a number of cancers including lung, breast, prostate and colorectal cancer.

IT 190795-31-4

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(nucleotide sequence, antisense DNA inhibiting checkpoint kinase

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gene expression; nucleic acid reagents for inhibition of  
checkpoint kinase-1 gene expression for therapeutic use)

L8 ANSWER 20 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:186701 HCAPLUS

DOCUMENT NUMBER: 135:57661

TITLE: Characterization in terms of the NUX rule of  
G-inserted mutant hammerhead ribozymes with high  
level of catalytic power

AUTHOR(S): Kuwabara, Tomoko; Warashina, Masaki; Kato,  
Yoshio; Kawasaki, Hiroaki; Taira, Kazunari

CORPORATE SOURCE: Gene Discovery Research Center, National  
Institute of Advanced Industrial Science and  
Technology (AIST), Tsukuba Science City,  
305-8562, Japan

SOURCE: Journal of Biochemistry and Molecular Biology  
(2001), 34(1), 51-58

CODEN: JBMBE5; ISSN: 1225-8687

PUBLISHER: Springer-Verlag Singapore Pte. Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Attempts using in vitro and in vivo selection procedures have been  
made to search for hammerhead ribozymes that have higher activities  
than the wild-type ribozyme and also to determine whether other sequences  
might be possible in the catalytic core of the hammerhead ribozyme.  
Active sequences selected in the past conformed broadly to the  
consensus core sequence except at A9, and no sequences were associated  
with higher activity than that of the hammerhead with the consensus  
core, an indication that the consensus sequence derived from viruses  
and virusoids is probably the optimal sequence. Recently, during  
construction of ribozyme expression vectors, we isolated a mutant  
hammerhead ribozyme, with an insertion of G between A9 and G10.1,  
that appeared to show significant activity. We, therefore,  
characterized kinetic properties of the G-inserted mutant ribozymes  
in terms of the NUX rule. We demonstrate that the NUX rule is  
basically applicable to the G-inserted ribozymes and, more  
importantly, one type of G-inserted ribozyme was very active with  
kcat value of 6.4 min<sup>-1</sup> in 50 mM Tris-HCl (pH 8.0) and 10 mM MgCl<sub>2</sub>  
at 37°C.

IT 345373-30-0 345373-31-1

RL: BAC (Biological activity or effector, except adverse); BSU  
(Biological study, unclassified); PRP (Properties); BIOL (Biological  
study)

(characterization in terms of the NUX rule of G-inserted mutant  
hammerhead ribozymes with high level of catalytic power)

REFERENCE COUNT: 91 THERE ARE 91 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L8 ANSWER 21 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:48059 HCAPLUS

DOCUMENT NUMBER: 134:291623

TITLE: In vitro-selected RNA cleaving DNA enzymes from  
a combinatorial library are potent inhibitors of  
HIV-1 gene expression

AUTHOR(S): Sriram, Bandi; Banerjee, Akhil C.

CORPORATE SOURCE: Laboratory of Virology, National Institute of  
Immunology, New Delhi, 110067, India

Searcher : Shears 571-272-2528

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SOURCE: Biochemical Journal (2000), 352(3), 667-673  
CODEN: BIJOAK; ISSN: 0264-6021  
PUBLISHER: Portland Press Ltd.  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB Selective inactivation of a target gene by antisense mechanisms is an important biol. tool to delineate specific functions of the gene product. Approaches mediated by ribozymes and RNA-cleaving DNA enzymes (DNA enzymes) are more attractive because of their ability to catalytically cleave the target RNA. DNA enzymes have recently gained a lot of importance because they are short DNA mols. with simple structures that are expected to be stable to the nucleases present inside a mammalian cell. The authors have designed a strategy to identify accessible cleavage sites in HIV-1 gag RNA from a pool of random DNA enzymes, and for isolation of DNA enzymes. A pool of random sequences (all 29 nucleotides long) that contained the earlier-identified 10-23 catalytic motif were tested for their ability to cleave the target RNA. When the pool of random DNA enzymes was targeted to cleave between any A and U nucleotides, DNA enzyme 1836 was identified. Although several DNA enzymes were identified using a pool of DNA enzymes that was completely randomized with respect to its substrate-binding properties, DNA enzyme-1810 was selected for further characterization. Both DNA enzymes showed target-specific cleavage activities in the presence of Mg<sup>2+</sup> only. When introduced into a mammalian cell, they showed interference with HIV-1-specific gene expression. This strategy could be applied for the selection of desired target sites in any target RNA.

IT 334544-13-7 334544-14-8

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(RNA-cleaving DNazymes from combinatorial library are potent inhibitors of HIV-1 gene expression)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 22 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:725799 HCAPLUS

DOCUMENT NUMBER: 133:291920

TITLE: Method for identifying antisense DNA-, ribozyme-, or DNazyme-accessible binding sites on RNA

INVENTOR(S): Rossi, John; Riggs, Arthur; Scherr, Michaela

PATENT ASSIGNEE(S): City of Hope, USA

SOURCE: PCT Int. Appl., 38 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000060115	A2	20001012	WO 2000-US7920	20000327
WO 2000060115	A3	20010426		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN,

Searcher : Shears 571-272-2528

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CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,  
HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,  
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT,  
RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,  
UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,  
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF,  
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 6562570 B1 20030513 US 2000-536393 20000328  
US 2003228615 A1 20031211 US 2003-435044 20030512  
PRIORITY APPLN. INFO.: US 1999-127529P P 19990402  
US 2000-536393 A1 20000328

AB A method for identifying sites on a target RNA which are accessible to pairing by antisense DNA, ribozymes or DNazymes. Native or in vitro -synthesized target RNA is incubated with defined ODNs and RNase H, or with a random or semi-random ODN library and RNase H, or with defined ribozymes or DNazymes, or with a semi-random ribozyme or DNazyme library, in a cell extract containing endogenous RNA binding proteins, or in a medium which mimics a cell extract due to presence of one or more RNA-binding proteins. Any antisense ODN, ribozyme or DNazyme which is complementary to an accessible site in the target RNA hybridizes to that site and the RNA is cleaved at that site. Reverse transcription can be used to generate a first strand DNA from the RNA cleavage product, and terminal deoxynucleotidyl transferase-dependent polymerase chain reaction (TDPCR) can be used to identify sites on target RNA to which antisense ODNs, ribozymes or DNazymes have bound and cleavage has occurred. The method was applied to identification of hammerhead ribozyme cleavage sites on human gene AIB1 mRNA as well as murine DNA methyltransferase mRNA.

IT 300756-64-3 300756-65-4

RL: PRP (Properties)

(unclaimed nucleotide sequence; method for identifying antisense DNA-, ribozyme-, or DNazyme-accessible binding sites on RNA)

L8 ANSWER 23 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:413290 HCAPLUS

DOCUMENT NUMBER: 133:234043

TITLE: Alternative Conformations of a Nucleic Acid  
Four-way Junction

AUTHOR(S): Nowakowski, Jacek; Shim, Peter J.; Stout, C.  
David; Joyce, Gerald F.

CORPORATE SOURCE: Department of Chemistry, Skaggs Institute for  
Chemical Biology, Scripps Research Institute, La  
Jolla, CA, 92037, USA

SOURCE: Journal of Molecular Biology (2000), 300(1),  
93-102

CODEN: JMOBAK; ISSN: 0022-2836

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A crystal structure of a 108 nucleotide RNA-DNA complex containing a four-way junction was solved at 3.1 Å resolution. The structure of the junction differs substantially from the "stacked-X" conformation observed previously, due to a 135° rotation of the branches. Comparison of the two conformers provides insight into the factors contributing to the flexibility of four-way junctions. The stacked-X conformation maximizes base-stacking but causes unfavorable repulsion between phosphate groups, whereas the 135

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°-rotated "crossed" conformation minimizes electrostatic clashes at the expense of reduced base-stacking. Despite the large rotation of the branches, both junction structures exhibit an antiparallel arrangement of the continuous strands and opposite polarity of the crossover strands. (c) 2000 Academic Press.

IT 292890-11-0

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(four-chain RNA-DNA complex; alternative conformations of a nucleic acid four-way junction)

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 24 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:124703 HCAPLUS

DOCUMENT NUMBER: 130:321986

TITLE: Crystal structure of an 82-nucleotide RNA-DNA complex formed by the 10-23 DNA enzyme

AUTHOR(S): Nowakowski, Jacek; Shim, Peter J.; Prasad, G. Sridhar; Stout, C. David; Joyce, Gerald F.

CORPORATE SOURCE: Department of Chemistry and The Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA, 92037, USA

SOURCE: Nature Structural Biology (1999), 6(2), 151-156  
CODEN: NSBIEW; ISSN: 1072-8368

PUBLISHER: Nature America

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The structure of a large nucleic acid complex formed by the 10-23 DNA enzyme bound to an RNA substrate was determined by x-ray diffraction at 3.0 Å resolution. The 82-nucleotide complex contains two strands of DNA and two strands of RNA that form five double-helical domains. The spatial arrangement of these helices is maintained by two four-way junctions that exhibit extensive base-stacking interactions and sharp turns of the phosphodiester backbone stabilized by metal ions coordinated to nucleotides at these junctions. Although it is unlikely that the structure corresponds to the catalytically active conformation of the enzyme, it represents a novel nucleic acid fold with implications for the Holliday junction structure.

IT 223694-53-9

RL: PRP (Properties)

(crystal structure of 82-nucleotide RNA-DNA complex formed by 10-23 DNA enzyme)

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 25 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1998:728600 HCAPLUS

DOCUMENT NUMBER: 130:1776

TITLE: Design and catalytic activity of enzymic DNA molecules

INVENTOR(S): Joyce, Gerald F.; Breaker, Ronald R.

PATENT ASSIGNEE(S): The Scripps Research Institute, USA

SOURCE: PCT Int. Appl., 161 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

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LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 1  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9849346	A1	19981105	WO 1998-US8677	19980429
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9872675	A1	19981124	AU 1998-72675	19980429
AU 735522	B2	20010712		
EP 981646	A1	20000301	EP 1998-920015	19980429
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
BR 9809433	A	20000613	BR 1998-9433	19980429
JP 2002514080	T2	20020514	JP 1998-547359	19980429
AU 743767	B2	20020207	AU 1999-65509	19991224
AU 9965509	A1	20000309		
PRIORITY APPLN. INFO.:			US 1997-45228P	P 19970429
			WO 1998-US8677	W 19980429
AB	<p>The present invention discloses DNA enzymes -- catalytic or enzymic DNA mols. -- capable of cleaving nucleic acid sequences or mols., particularly RNA, in a site-specific manner, as well as compns. including same. The catalytic DNAs have first and substrate binding regions flanks a core region, wherein the first substrate binding region has a sequence complementary to a first portion of the preselected substrate nucleic acid sequence, and the second substrate binding region has a sequence complementary to a second portion of the preselected substrate nucleic acid sequence. The core region has a sequence according to the formula T(stem)'AGC(stem)"Z, where the (stem)' and (stem)" are each 3 sequential nucleotides which when hybridized as a (stem)':(stem)" pair comprise 3 base pairs including at least two G:C pairs and wherein Z = WCGR or WCGAA, and W = A or T and R = A or G. Also contemplated is a core region having a sequence RGGCTAGCXACAACGA, wherein X = T, C or A, and R = A or G. Methods of making and using the disclosed enzymes and compns. are also disclosed. An exemplary method of engineering enzymic DNA mols. that cleave phosphoester bonds comprises the following in vitro selection/evolution steps: (1) obtaining a population of single-stranded DNA mols.; (2) introducing genetic variation into the population to produce a variant population; (3) selecting individuals from the variant population that meet predetd. selection criteria; (4) separating the selected individuals from the remainder of the variant population; and (5) amplifying the selected individuals. Deoxyribozymes variants designated 8-17 (core region 5'-cttccaccttccgagccggaagttactttt-3') and 10-23 (core region 5'-ctttggttaggctagctacaacgatttttcc-3') have turnover nos. and kobs of 0.5 and 1 h-1, 0.002 and 0.01 min-1, resp., in 10 mM Mg2+, pH 7.5 and 37°.</p>			
IT	215727-35-8P, Deoxyribozyme (synthetic clone 10-38)			

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RL: BAC (Biological activity or effector, except adverse); BPN  
(Biosynthetic preparation); BSU (Biological study, unclassified);  
PRP (Properties); BIOL (Biological study); PREP (Preparation)  
(design and catalytic activity of enzymic DNA mols.)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR  
THIS RECORD. ALL CITATIONS AVAILABLE IN  
THE RE FORMAT

L8 ANSWER 26 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1997:308152 HCAPLUS

DOCUMENT NUMBER: 127:30832

TITLE: A general purpose RNA-cleaving DNA enzyme

AUTHOR(S): Santoro, Stephen W.; Joyce, Gerald F.

CORPORATE SOURCE: Departments of Chemistry and Molecular Biology  
and the Skaggs Institute for Chemical Biology,  
The Scripps Research Institute, La Jolla, CA,  
92037, USA

SOURCE: Proceedings of the National Academy of Sciences  
of the United States of America (1997), 94(9),  
4262-4266

CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An in vitro selection procedure was used to develop a DNA enzyme  
that can be made to cleave almost any targeted RNA substrate under  
simulated physiol. conditions. The enzyme is comprised of a  
catalytic domain of 15 deoxynucleotides, flanked by two  
substrate-recognition domains of seven to eight deoxynucleotides  
each. The RNA substrate is bound through Watson-Crick base pairing  
and is cleaved at a particular phosphodiester located between an  
unpaired purine and a paired pyridine residue. Despite its small  
size, the DNA enzyme has a catalytic efficiency ( $K_{cat}/K_m$ ) of  
 $\approx 10^9$  M<sup>-1</sup>min<sup>-1</sup> under multiple turnover conditions, exceeding  
that of any other known nucleic acid enzyme. Its activity is  
dependent on the presence of Mg<sup>2+</sup> ion. By changing the sequence of  
the substrate-recognition domains, the DNA enzyme can be made to  
target different RNA substrates. In this study, for example, it was  
directed to cleave synthetic RNAs corresponding to the start codon  
region of HIV-1 gag/pol, env, vpr, tat, and nef mRNAs.

IT 190795-31-4

RL: BAC (Biological activity or effector, except adverse); BPR  
(Biological process); BSU (Biological study, unclassified); RCT  
(Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant  
or reagent)

(general purpose RNA-cleaving DNA enzyme)

E1 THROUGH E28 ASSIGNED

FILE 'REGISTRY' ENTERED AT 12:41:44 ON 21 JAN 2004

L9 28 SEA FILE=REGISTRY ABB=ON PLU=ON (190795-31-4/BI OR  
215727-35-8/BI OR 223694-53-9/BI OR 292890-11-0/BI OR  
300756-64-3/BI OR 300756-65-4/BI OR 334544-13-7/BI OR  
334544-14-8/BI OR 345373-30-0/BI OR 345373-31-1/BI OR  
400185-65-1/BI OR 403777-66-2/BI OR 444035-98-7/BI OR  
478129-01-0/BI OR 479786-61-3/BI OR 483392-16-1/BI OR  
484802-52-0/BI OR 491672-93-6/BI OR 493068-33-0/BI OR  
503875-66-9/BI OR 504513-55-7/BI OR 506617-43-2/BI OR

Searcher : Shears 571-272-2528

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09/423035

543745-67-1/BI OR 557143-59-6/BI OR 591261-44-8/BI OR  
613321-58-7/BI OR 633370-08-8/BI OR 638223-95-7/BI)

L10 28 S L9 AND L1

L10 ANSWER 1 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 638223-95-7 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====   
HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

L10 ANSWER 2 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 633370-08-8 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 12: PN: US20030228590 SEQID: 14 unclaimed DNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====   
HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 140:26917

L10 ANSWER 3 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 613321-58-7 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 2617: PN: US20030203870 SEQID: 2617 unclaimed DNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====   
HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 139:317479

L10 ANSWER 4 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 591261-44-8 REGISTRY  
CN DNA, d(N-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 63: PN: US2003171311 SEQID: 9700 unclaimed DNA  
CI MAN  
SQL 16

Searcher : Shears 571-272-2528

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SEQ 1 nggctagcta caacga

=====

HITS AT: 1-16

REFERENCE 1: 139:224402

L10 ANSWER 5 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 557143-59-6 REGISTRY

CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1913: PN: US20030125270 FIGURE: 5 unclaimed DNA

CI MAN

SQL 16

SEQ 1 rggctagcta caacga

=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 139:358722

L10 ANSWER 6 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 543745-67-1 REGISTRY

CN DNA, d(A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-(3'→3')-G) (9CI) (CA INDEX NAME)

CI MAN

SQL 17

SEQ 1 aggctagcta caacgag

=====

HITS AT: 1-16

REFERENCE 1: 139:46323

L10 ANSWER 7 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 506617-43-2 REGISTRY

CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 4771: PN: US20030073207 SEQID: 9645 unclaimed DNA

CI MAN

SQL 16

SEQ 1 rggctagcta caacga

=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 139:143909

L10 ANSWER 8 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 504513-55-7 REGISTRY

CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 21: PN: US20030065155 SEQID: 21 unclaimed DNA

CI MAN

SQL 16

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09/423035

SEQ 1 rggctagcta caacga  
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HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:282290

L10 ANSWER 9 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 503875-66-9 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 445: PN: US20030064945 SEQID: 445 claimed DNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:292713

L10 ANSWER 10 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 493068-33-0 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 13: PN: WO03008628 SEQID: 13 unclaimed DNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:142441

L10 ANSWER 11 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 491672-93-6 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 1774: PN: WO02081494 SEQID: 16197 unclaimed DNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:314544

L10 ANSWER 12 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

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RN 484802-52-0 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 80: PN: WO02081628 SEQID: 13274 unclaimed DNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====   
HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:265678

L10 ANSWER 13 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 483392-16-1 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 21: PN: US20030008295 SEQID: 21 unclaimed DNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====   
HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:84437

L10 ANSWER 14 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479786-61-3 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 2122: PN: WO02068637 SEQID: 37054 unclaimed RNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====   
HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:66656

L10 ANSWER 15 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 478129-01-0 REGISTRY  
CN DNA, d(Y-R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-R) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 1332: PN: WO02097114 SEQID: 6810 unclaimed RNA  
CI MAN  
SQL 18

SEQ 1 yrggctagct acaacgar  
=====   
HITS AT: 2-17

Searcher : Shears 571-272-2528

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REFERENCE 1: 138:19530

L10 ANSWER 16 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 444035-98-7 REGISTRY  
CN DNA, d(G-A-G-C-T-G-G-A-G-G-A-A-A-C-G-G-C-A-G-T-C), complex with DNA  
d(G-G-G-C-A-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-A-A-A-T-T-G-G-A-G-G-  
A-A-G-C-T-C) and RNA (G-A-C-U-G-C-C-G-U-A-G-G-U-U-G-C-C-C) (1:1:1)  
(9CI) (CA INDEX NAME)  
CI MAN  
SQL 78,39,21,18

SEQ 1 gggcaaggct agctacaacg actaaattgg aggaagctc  
=====

HITS AT: 6-21

SEQ 1 gagctggagg aaacggcagt c

SEQ 1 gacugccgua gguugccc

REFERENCE 1: 137:121425

L10 ANSWER 17 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 403777-66-2 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 136:241681

L10 ANSWER 18 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 400185-65-1 REGISTRY  
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 449: PN: WO0211674 SEQID: 5447 unclaimed DNA  
CI MAN  
SQL 16

SEQ 1 rggctagcta caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 136:194272

L10 ANSWER 19 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 345373-31-1 REGISTRY  
CN DNA, d(A-T-C-T-T-G-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-A-C-C-A-T-G),  
complex with RNA (C-A-U-G-G-U-A-C-A-A-G-A-U) (1:1) (9CI) (CA INDEX  
NAME)  
OTHER CA INDEX NAMES:

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CN RNA, (C-A-U-G-G-U-A-C-A-A-G-A-U), complex with DNA  
d(A-T-C-T-T-G-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-A-C-C-A-T-G) (1:1) (9CI)  
CI MAN  
SQL 40,27,13

SEQ 1 atcttgggct agctacaacg aaccatg  
=====

HITS AT: 6-21

SEQ 1 caugguacaa gau

REFERENCE 1: 135:57661

L10 ANSWER 20 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 345373-30-0 REGISTRY

CN DNA, d(C-G-G-A-G-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-A-C-A-A-G-C),  
complex with RNA (G-C-U-U-G-U-A-U-C-U-C-C-G) (1:1) (9CI) (CA INDEX  
NAME)

OTHER CA INDEX NAMES:

CN RNA, (G-C-U-U-G-U-A-U-C-U-C-C-G), complex with DNA  
d(C-G-G-A-G-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-A-C-A-A-G-C) (1:1) (9CI)

CI MAN

SQL 40,27,13

SEQ 1 cggagaggct agctacaacg aacaagc  
=====

HITS AT: 6-21

SEQ 1 gcuuguaucu ccg

REFERENCE 1: 135:57661

L10 ANSWER 21 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 334544-14-8 REGISTRY

CN DNA, d(A-G-T-G-T-C-G-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-T-C-C-T-G-G-T),  
complex with RNA (A-C-C-A-G-G-A-G-C-G-A-C-A-C-U) (1:1) (9CI) (CA  
INDEX NAME)

OTHER CA INDEX NAMES:

CN RNA, (A-C-C-A-G-G-A-G-C-G-A-C-A-C-U), complex with DNA  
d(A-G-T-G-T-C-G-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-T-C-C-T-G-G-T) (1:1)  
(9CI)

CI MAN

SQL 44,29,15

SEQ 1 agtgtcgggc tagctacaac gatcctggt  
=====

HITS AT: 7-22

SEQ 1 accaggagcg acacu

REFERENCE 1: 134:291623

L10 ANSWER 22 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 334544-13-7 REGISTRY

CN DNA, d(C-C-T-G-A-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-G-C-T-G-T-C-A),  
complex with RNA (U-G-A-C-A-G-C-A-U-G-U-C-A-G-G) (1:1) (9CI) (CA  
INDEX NAME)

OTHER CA INDEX NAMES:

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CN RNA, (U-G-A-C-A-G-C-A-U-G-U-C-A-G-G), complex with DNA  
d(C-C-T-G-A-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-G-C-T-G-T-C-A) (1:1)  
(9CI)

CI MAN  
SQL 44,29,15

SEQ 1 cctgacaggc tagctacaac gagctgtca  
=====

HITS AT: 7-22

SEQ 1 ugacagcaug ucagg

REFERENCE 1: 134:291623

L10 ANSWER 23 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 300756-65-4 REGISTRY

CN 14: PN: WO0060115 SEQID: 20 unclaimed DNA (9CI) (CA INDEX NAME)

CI MAN

SQL 16

SEQ 1 gggctagcta caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 133:291920

L10 ANSWER 24 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 300756-64-3 REGISTRY

CN 13: PN: WO0060115 SEQID: 19 unclaimed DNA (9CI) (CA INDEX NAME)

CI MAN

SQL 16

SEQ 1 aggctagcta caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 133:291920

L10 ANSWER 25 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 292890-11-0 REGISTRY

CN DNA, d(C-T-C-G-C-A-C-C-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-C-T-C-T-C-T-C-C-T), complex with RNA (A-G-G-A-G-A-G-A-G-A-U-G-G-G-U-G-C-G-A-G) (1:1) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN RNA, (A-G-G-A-G-A-G-A-G-A-U-G-G-G-U-G-C-G-A-G), complex with DNA  
d(C-T-C-G-C-A-C-C-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-C-T-C-T-C-C-T) (1:1) (9CI)

OTHER NAMES:

CN DNA (synthetic DNA-RNA four-way junction)

CN DNA (synthetic DNA-RNA Holliday junction)

CI MAN

SQL 54,34,20

SEQ 1 ctcgcaccca ggctagctac aacgactctc tcct

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HITS AT: 10-25

SEQ 1 aggagagaga ugggugcgag

REFERENCE 1: 133:234043

L10 ANSWER 26 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 223694-53-9 REGISTRY

CN DNA, d(G-C-T-C-C-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-G-T-C-C),  
complex with RNA (G-G-A-C-A-G-A-U-G-G-G-A-G) (1:1) (9CI) (CA INDEX  
NAME)

OTHER CA INDEX NAMES:

CN RNA, (G-G-A-C-A-G-A-U-G-G-G-A-G), complex with DNA  
d(G-C-T-C-C-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-G-T-C-C) (1:1)  
(9CI)

CI MAN

SQL 82,28,28,13,13

SEQ 1 gctcccaggc tagctacaac gactgtcc  
=====

HITS AT: 7-22

SEQ 1 gctcccaggc tagctacaac gactgtcc  
=====

HITS AT: 7-22

SEQ 1 ggacagaugg gag

SEQ 1 ggacagaugg gag

REFERENCE 1: 130:321986

L10 ANSWER 27 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 215727-35-8 REGISTRY

CN Deoxyribozyme (synthetic clone 10-38) (9CI) (CA INDEX NAME)

CI MAN

SQL 16

SEQ 1 rggctagcha caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 130:1776

L10 ANSWER 28 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 190795-31-4 REGISTRY

CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)

CI MAN

SQL 16

SEQ 1 rggctagcta caacga  
=====

HITS AT: 1-16

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

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REFERENCE 1: 135:175355

REFERENCE 2: 127:30832

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:26:43 ; Search time 1380 Seconds  
(without alignments)  
281.791 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16

Sequence: 1 rgcgtagctacaacga 16

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 452990

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :

EST:\*  
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2: em\_estbun:\*  
3: em\_estlin:\*  
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6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hnc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hnc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
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19: em\_gss\_pln:\*  
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22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vit1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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4	12	75.0	26	28	BH901408	BH901408 SALK_0790

5	12	75.0	75	13	BH866082	BH866082 S062E01 P
6	12	75.0	95	13	BH867160	BH867160 S075A07 P
7	12	75.0	96	13	BH862306	BH862306 S014A04 P
8	12	75.0	100	13	BH861867	BH861867 S007G10 P
9	11.6	72.5	80	28	AZ619815	AZ619815 1M0452D18
10	11.4	71.2	52	14	H08942	H08942 Y193e05.r1
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12	11.4	71.2	76	29	BX535085	BX535085 Arabidops
13	11.4	71.2	95	9	A1461140	A1461140 B875F01.Y
14	11.4	71.2	95	13	BQ823860	BQ823860 1030113D0
15	11.4	71.2	96	28	AZ916132	AZ916132 Pat1_3_ab
16	11.4	71.2	58	29	BX288422	BX288422 Arabidops
17	11	68.8	73	14	H62825	H62825 Y146G04.s1
18	11	68.8	82	12	B1865456	B1865456 f22h12.x
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21	11	68.8	90	28	BH861753	BH861753 SALK_0879
22	11	68.8	91	29	AG224693	AG224693 locut_jap
23	11	68.8	96	28	AZ431360	AZ431360 1M0216F14
24	11	68.8	49	9	A1681141	A1681141 tx44d07.x
25	10.8	67.5	50	9	AU106358	AU106358 AU106358
26	10.8	67.5	52	9	AA425092	AA425092 zw11f11.r
27	10.8	67.5	52	29	BZ765391	BZ765391 SALK_1311
28	10.8	67.5	58	9	AA433099	AA433099 v04e08.r
29	10.8	67.5	59	28	AZ342599	AZ342599 1M0075C18
30	10.8	67.5	60	29	CNS0682T	AL394587 T3 end of
31	10.8	67.5	61	9	AA070413	AA070413 zme8c11.r
32	10.8	67.5	62	14	D12015	D12015 HUM0005149
33	10.8	67.5	65	9	AA499456	AA499456 v185904.r
34	10.8	67.5	65	28	BH414369	BH414369 1007037G0
35	10.8	67.5	65	29	TA184A08Q	TA184A08Q
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37	10.8	67.5	67	9	AA771119	AA771119 vt16h01.r
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41	10.8	67.5	72	28	BH911226	BH911226 SALK_0670
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67	10.8	67.5	94	9	AA435359	AA435359 ve15e06.r
68	10.8	67.5	94	9	AA512503	AA512503 vj17h04.r
69	10.8	67.5	94	29	BZ291056	BZ291056 SALK_1123
70	10.8	67.5	94	29	AG219003	AG219003 Drosoph11
71	10.8	67.5	95	9	AA919502	AA919502 vz20g11.r
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C 83	10.8	67.5	99	10	BG695449	BG695449	156	10.4	65.0	93	10	BG409079	BG409079
C 84	10.8	67.5	99	12	BI421049	BI421049	157	10.4	65.0	93	29	AL752909	AL752909
C 85	10.8	67.5	99	28	BH418153	BH418153	158	10.4	65.0	93	29	AL753208	AL753208
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C 88	10.8	67.5	100	10	BF874679	BF874679	161	10.4	65.0	94	29	AZ508999	AZ508999
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C 91	10.6	66.2	93	13	BO766868	BO766868	164	10.4	65.0	98	10	AM596808	AM596808
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C 96	10.4	65.0	43	28	AZ502070	AZ502070	169	10.4	65.0	99	28	BH214808	BH214808
C 97	10.4	65.0	43	29	AL755953	AL755953	170	10.4	65.0	100	9	AM797834	AM797834
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C 99	10.4	65.0	49	28	BH861777	BH861777	172	10.2	63.7	42	10	BF527907	BF527907
C 100	10.4	65.0	49	28	BH861778	BH861778	173	10.2	63.7	53	28	AZ625652	AZ625652
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C 104	10.4	65.0	53	9	AI161613	AI161613	177	10.2	63.7	68	9	AU256518	AU256518
C 105	10.4	65.0	53	9	AM102062	AM102062	178	10.2	63.7	68	28	BH644273	BH644273
C 106	10.4	65.0	53	14	H18867	H18867	179	10.2	63.7	74	29	CC1179318	CC1179318
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C 108	10.4	65.0	54	29	AL756050	AL756050	181	10.2	63.7	76	10	BE058589	BE058589
C 109	10.4	65.0	55	9	AA142563	AA142563	182	10.2	63.7	79	14	U44372	U44372
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C 111	10.4	65.0	63	28	AZ435853	AZ435853	184	10.2	63.7	82	9	AA594999	AA594999
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C 114	10.4	65.0	66	28	BH894070	BH894070	187	10.2	63.7	86	9	AA236075	AA236075
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C 116	10.4	65.0	67	28	BH908636	BH908636	189	10.2	63.7	91	14	CB394112	CB394112
C 117	10.4	65.0	69	29	AL752981	AL752981	190	10.2	63.7	91	28	BH851397	BH851397
C 118	10.4	65.0	70	29	AL753206	AL753206	191	10.2	63.7	92	28	AZ778554	AZ778554
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C 126	10.4	65.0	76	29	AL753252	AL753252	199	10.2	63.7	33	29	BZ358119	BZ358119
C 127	10.4	65.0	76	29	HA8275805	HA8275805	200	10.2	63.7	37	9	AA864329	AA864329
C 128	10.4	65.0	77	14	CA819431	CA819431	201	10.2	63.7	37	9	AA985715	AA985715
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C 131	10.4	65.0	80	9	AL820251	AL820251	204	10.2	63.7	43	28	AZ789583	AZ789583
C 132	10.4	65.0	81	13	BO823042	BO823042	205	10.2	63.7	46	28	BH635864	BH635864
C 133	10.4	65.0	81	29	CC457634	CC457634	206	10.2	63.7	47	29	TA359H02	TA359H02
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C 139	10.4	65.0	84	9	AM722919	AM722919	212	10.2	63.7	58	9	AI195289	AI195289
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C 141	10.4	65.0	85	9	AV842614	AV842614	214	10.2	63.7	58	12	BI944444	BI944444
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C 143	10.4	65.0	88	28	BH228507	BH228507	216	10.2	63.7	60	29	BF471331	BF471331
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C 146	10.4	65.0	90	9	AI120073	AI120073	219	10.2	63.7	65	9	AI926212	AI926212
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C 148	10.4	65.0	90	13	D20584	D20584	221	10.2	63.7	68	10	BE463636	BE463636
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C 683	9.4	58.8	91	14	W35852	C 756	9.2	57.5	23	28	AZ303987
C 684	9.4	58.8	91	28	BH216058	C 757	9.2	57.5	24	11	CNS08018
C 685	9.4	58.8	92	9	AT000234	C 758	9.2	57.5	26	29	BZ358021
C 686	9.4	58.8	92	10	BF676997	C 759	9.2	57.5	27	28	AZ799014
C 687	9.4	58.8	92	14	CB006075	C 760	9.2	57.5	28	28	BH911462
C 688	9.4	58.8	92	14	CB402602	C 761	9.2	57.5	30	10	BE278221
C 689	9.4	58.8	92	28	AZ131080	C 762	9.2	57.5	30	10	BE278715
C 690	9.4	58.8	92	28	BH217859	C 763	9.2	57.5	30	10	BE385997
C 691	9.4	58.8	92	29	BZ764434	C 764	9.2	57.5	30	10	BE386027
C 692	9.4	58.8	92	29	AG220799	C 765	9.2	57.5	30	10	BE386094
C 693	9.4	58.8	92	29	AG257737	C 766	9.2	57.5	30	10	BE389637
C 694	9.4	58.8	92	29	AL770432	C 767	9.2	57.5	30	10	BE900457
C 695	9.4	58.8	93	9	AV909387	C 768	9.2	57.5	30	28	BH909028
C 696	9.4	58.8	93	14	CB827185	C 769	9.2	57.5	31	10	BE274171
C 697	9.4	58.8	93	28	BH848820	C 770	9.2	57.5	31	10	BE277749
C 698	9.4	58.8	93	29	BZ383142	C 771	9.2	57.5	31	10	BE280621
C 699	9.4	58.8	93	29	BX201107	C 772	9.2	57.5	31	10	BE298405
C 700	9.4	58.8	94	9	AA215254	C 773	9.2	57.5	31	10	BE388076
C 701	9.4	58.8	94	28	AZ920726	C 774	9.2	57.5	31	10	BE408963
C 702	9.4	58.8	95	12	BM306418	C 775	9.2	57.5	32	10	BE729734
C 703	9.4	58.8	95	12	BM306418	C 776	9.2	57.5	32	29	TA227H06Q
C 704	9.4	58.8	95	28	AZ388579	C 777	9.2	57.5	33	10	BF025659
C 705	9.4	58.8	96	9	AA845963	C 778	9.2	57.5	33	10	BE296540
C 706	9.4	58.8	96	9	AI869450	C 779	9.2	57.5	34	10	BE298772
C 707	9.4	58.8	96	28	AZ432614	C 780	9.2	57.5	34	10	BE389902
C 708	9.4	58.8	97	10	BF426038	C 781	9.2	57.5	34	28	AZ810771
C 709	9.4	58.8	97	13	BF426038	C 782	9.2	57.5	35	10	BE385175
C 710	9.4	58.8	97	14	CH356166	C 783	9.2	57.5	35	10	BE409354
C 711	9.4	58.8	97	14	H48944	C 784	9.2	57.5	35	28	AZ430239
C 712	9.4	58.8	97	14	HA8944	C 785	9.2	57.5	35	28	BH911899
C 713	9.4	58.8	97	28	AZ598831	C 786	9.2	57.5	36	28	BH911900
C 714	9.4	58.8	97	29	AG261655	C 787	9.2	57.5	36	28	BH911900
C 715	9.4	58.8	97	29	DR33J12T	C 788	9.2	57.5	37	28	AZ873706
C 716	9.4	58.8	98	9	AL829985	C 789	9.2	57.5	37	28	BE732314
C 717	9.4	58.8	98	9	AV525314	C 790	9.2	57.5	38	28	AZ660837
C 718	9.4	58.8	98	14	Z20006	C 791	9.2	57.5	38	28	AZ660837
C 719	9.4	58.8	98	29	CNS0336B	C 792	9.2	57.5	38	28	AZ806182
C 720	9.4	58.8	99	9	AJ499407	C 793	9.2	57.5	38	28	AZ806182
C 721	9.4	58.8	99	9	AL957894	C 794	9.2	57.5	38	28	AZ806182
C 722	9.4	58.8	99	10	BF80707	C 795	9.2	57.5	39	14	AG020646
C 723	9.4	58.8	99	10	BF850128	C 796	9.2	57.5	40	9	AI959899
C 724	9.4	58.8	99	12	BM942335	C 797	9.2	57.5	40	9	AA199679
C 725	9.4	58.8	99	12	BM981655	C 798	9.2	57.5	40	9	AA199679
C 726	9.4	58.8	99	14	R88374	C 799	9.2	57.5	40	9	AA199679
C 727	9.4	58.8	99	28	BH901247	C 800	9.2	57.5	40	29	AL994126
C 728	9.4	58.8	99	28	BH901247	C 801	9.2	57.5	41	28	AL994126
C 729	9.4	58.8	99	29	AG255479	C 802	9.2	57.5	41	28	AL994126
C 730	9.4	58.8	99	29	AG255479	C 803	9.2	57.5	41	29	BE762859
C 731	9.4	58.8	100	9	AA013890	C 804	9.2	57.5	41	29	BE762859
C 732	9.4	58.8	100	9	AA013890	C 805	9.2	57.5	42	9	AV833522
C 733	9.4	58.8	100	9	AI558976	C 806	9.2	57.5	42	10	BF206391
C 734	9.4	58.8	100	9	AA175673	C 807	9.2	57.5	42	28	AZ649663

808	9.2	57.5	42	29	AL947757	ArabiDops	C 881	9.2	57.5	54	10	BE022588	BE022588 sm6h08.y
809	9.2	57.5	43	9	AA948228	ocq2h1.s	C 882	9.2	57.5	54	12	BI261027	BI261027 6012972214
810	9.2	57.5	43	9	AI795121	bb7ra1.y	C 883	9.2	57.5	54	13	BQ592460	BQ592460 6023668-0
811	9.2	57.5	43	9	AW566030	EST00022	C 884	9.2	57.5	54	28	BH906886	BH906886 SALK_0362
812	9.2	57.5	43	28	AZ349590	1M0086H09	C 885	9.2	57.5	54	29	BZ769887	BZ769887 SALK_1428
813	9.2	57.5	44	10	BF102281	601752583	C 886	9.2	57.5	54	29	DR102823T	DR102823T
814	9.2	57.5	44	14	CA907055	PCSC06467	C 887	9.2	57.5	55	9	AM306630	AM306630 se53c11.y
815	9.2	57.5	44	14	M65525	EST083_chic	C 888	9.2	57.5	55	13	BU068713	BU068713 2565.G01
816	9.2	57.5	44	28	AZ470514	1M0284E10	C 889	9.2	57.5	55	29	AL753005	AL753005 ArabiDops
817	9.2	57.5	44	29	AL764168	ArabiDops	C 890	9.2	57.5	55	29	BX204435	BX204435 Danilo rer
818	9.2	57.5	46	9	AA756346	ah65h06.s	C 891	9.2	57.5	56	9	AA906034	AA906034 o350b02.s
819	9.2	57.5	46	9	AA789691	cg32c10.s	C 892	9.2	57.5	56	10	BE280329	BE280329 601157870
820	9.2	57.5	47	9	AU012362	AU012362	C 893	9.2	57.5	56	14	CB274974	CB274974 kg74h09.y
821	9.2	57.5	47	9	AU012362	AU012362	C 894	9.2	57.5	56	28	AZ645965	AZ645965 1M0511E17
822	9.2	57.5	47	28	BH891856	3526_119	C 895	9.2	57.5	56	28	BH852317	BH852317 SALK_0744
823	9.2	57.5	47	28	BH891856	3526_119	C 896	9.2	57.5	56	28	BZ663353	BZ663353 SALK_0269
824	9.2	57.5	48	28	AZ639981	1M0501D16	C 897	9.2	57.5	57	13	BQ382141	BQ382141 Kk42902.y
825	9.2	57.5	48	29	AG218322	Drcosphil	C 898	9.2	57.5	57	13	BQ382493	BQ382493 Kk51d04.y
826	9.2	57.5	48	29	BX209797	Danio rer	C 899	9.2	57.5	57	14	M00883	M00883 za55a02.x1
827	9.2	57.5	49	9	AI200287	qf6ba10.x	C 900	9.2	57.5	57	29	BZ762555	BZ762555 SALK_1053
828	9.2	57.5	49	28	AZ586447	1M0392B22	C 901	9.2	57.5	58	9	AI208634	AI208634 q934b06.x
829	9.2	57.5	50	9	AU103863	AU103863	C 902	9.2	57.5	58	9	AA138639	AA138639 mte2d11.x
830	9.2	57.5	50	9	AU103864	AU103864	C 903	9.2	57.5	58	9	AI453341	AI453341 t377a08.x
831	9.2	57.5	50	9	AU103865	AU103865	C 904	9.2	57.5	58	9	AA458540	AA458540 sh10d12.y
832	9.2	57.5	50	9	AU103867	AU103867	C 905	9.2	57.5	58	10	BE733638	BE733638 601567537
833	9.2	57.5	50	9	AU103870	AU103870	C 906	9.2	57.5	58	12	BI493871	BI493871 df106409.y
834	9.2	57.5	50	9	AU103874	AU103874	C 907	9.2	57.5	58	14	CB003153	CB003153 VVB027A03
835	9.2	57.5	50	9	AU103875	AU103875	C 908	9.2	57.5	58	14	CB003932	CB003932 VVB030H05
836	9.2	57.5	50	9	AU103876	AU103876	C 909	9.2	57.5	58	28	AZ591317	AZ591317 1M0401B24
837	9.2	57.5	50	9	AU103877	AU103877	C 910	9.2	57.5	58	28	AZ917758	AZ917758 1006002A0
838	9.2	57.5	50	9	AU103880	AU103880	C 911	9.2	57.5	58	29	AL942095	AL942095 ArabiDops
839	9.2	57.5	50	9	AU103881	AU103881	C 912	9.2	57.5	58	29	DR4B12S	DR4B12S Danilo rer
840	9.2	57.5	50	9	AU103883	AU103883	C 913	9.2	57.5	58	29	TA113A05Q	TA113A05Q
841	9.2	57.5	50	9	AU103885	AU103885	C 914	9.2	57.5	59	9	AI451268	AI451268 mte7c01.x
842	9.2	57.5	50	9	AU103892	AU103892	C 915	9.2	57.5	59	10	BP013445	BP013445 kR8f04.y
843	9.2	57.5	50	9	AU103893	AU103893	C 916	9.2	57.5	59	28	AQ254664	AQ254664 BP(3)0887
844	9.2	57.5	50	9	AU104305	AU104305	C 917	9.2	57.5	60	9	AM719257	AM719257 LjNESTR96
845	9.2	57.5	50	9	AU104386	AU104386	C 918	9.2	57.5	60	14	CB277341	CB277341 ku64c10.y
846	9.2	57.5	50	9	AU104387	AU104387	C 919	9.2	57.5	60	14	CD028775	CD028775 mte8002xH
847	9.2	57.5	50	9	AU104486	AU104486	C 920	9.2	57.5	60	28	BH865304	BH865304 SALK_0981
848	9.2	57.5	50	9	AU105006	AU105006	C 921	9.2	57.5	60	29	CC199567	CC199567 XE809 Bay
849	9.2	57.5	50	9	AU105969	AU105969	C 922	9.2	57.5	60	29	CC457394	CC457394 SALK_1096
850	9.2	57.5	50	9	AU107634	AU107634	C 923	9.2	57.5	60	29	BX535184	BX535184 ArabiDops
851	9.2	57.5	50	9	AU108086	AU108086	C 924	9.2	57.5	60	29	DR102D22S	DR102D22S Danilo rer
852	9.2	57.5	50	12	BJ035910	BJ035910	C 925	9.2	57.5	61	9	AU012625	AU012625
853	9.2	57.5	50	14	CB218569	NISC_nb09	C 926	9.2	57.5	61	9	AA581081	AA581081 nd13b07.s
854	9.2	57.5	50	14	T73299	yc34b09.s1	C 927	9.2	57.5	61	14	AA586727	AA586727 mte7c10.s
855	9.2	57.5	50	29	BZ766844	SALK_1379	C 928	9.2	57.5	61	13	BQ079624	BQ079624 aa116b05.y
856	9.2	57.5	50	29	TA187C12P	AL477525 T_btuce1	C 929	9.2	57.5	61	14	CB016864	CB016864 pmc.pko
857	9.2	57.5	51	9	AI873986	AI873986	C 930	9.2	57.5	62	10	BE278269	BE278269 601179416
858	9.2	57.5	51	9	AM156250	se21e05.y	C 931	9.2	57.5	62	13	BQ595222	BQ595222 E012711-0
859	9.2	57.5	51	28	AZ594400	1M0406K23	C 932	9.2	57.5	62	28	AZ920963	AZ920963 1006023A0
860	9.2	57.5	51	28	BH225854	1006128G0	C 933	9.2	57.5	62	28	BH219720	BH219720 1006090B0
861	9.2	57.5	51	28	BH861528	SALK_0817	C 934	9.2	57.5	62	29	BZ355855	BZ355855 SALK_1276
862	9.2	57.5	51	29	AL944876	ArabiDops	C 935	9.2	57.5	62	29	BZ380489	BZ380489 SALK_1152
863	9.2	57.5	52	9	AA068274	mm53c01.t	C 936	9.2	57.5	62	29	BZ764789	BZ764789 SALK_1269
864	9.2	57.5	52	9	AA723687	ah85c05.s	C 937	9.2	57.5	62	29	AL762933	AL762933 ArabiDops
865	9.2	57.5	52	9	AI143632	qb74c03.x	C 938	9.2	57.5	63	9	AM396172	AM396172 sh25g09.y
866	9.2	57.5	52	9	AM693197	NF063B11S	C 939	9.2	57.5	63	13	BQ636245	BQ636245 h406d03.y
867	9.2	57.5	52	9	AA499863	vg05g12.r	C 940	9.2	57.5	63	28	AZ836154	AZ836154 2M0130A20
868	9.2	57.5	52	12	BJ075938	BJ075938	C 941	9.2	57.5	63	29	BZ291038	BZ291038 SALK_1123
869	9.2	57.5	52	28	AZ495807	1M0331F21	C 942	9.2	57.5	63	29	BZ381526	BZ381526 SALK_1168
870	9.2	57.5	52	29	BZ769876	SALK_1428	C 943	9.2	57.5	64	9	AI1221064	AI1221064 qg90d10.x
871	9.2	57.5	52	29	CC248941	KX287 Bay	C 944	9.2	57.5	64	9	AM55202.x	AM55202.x
872	9.2	57.5	53	13	BQ382839	kK56h09.y	C 945	9.2	57.5	64	9	AM620167	AM620167 SMOVAFCAP
873	9.2	57.5	53	14	CA910469	PCSC08867	C 946	9.2	57.5	64	9	AA626441	AA626441 SMOVAFCAP
874	9.2	57.5	53	14	CB274957	ku73c02.y	C 947	9.2	57.5	64	9	AA432439	AA432439 v032e11.x
875	9.2	57.5	53	14	R884455	ym92d07.r1	C 948	9.2	57.5	64	9	AA572476	AA572476 v182d11.x
876	9.2	57.5	53	28	AZ353396	1M0092F18	C 949	9.2	57.5	64	9	AA572477	AA572477 v182d12.x
877	9.2	57.5	53	28	AZ442528	1M0236H08	C 950	9.2	57.5	64	11	CN609MTR	CN609MTR
878	9.2	57.5	53	28	BH790547	SALK_0573	C 951	9.2	57.5	64	11	BI097356	BI097356 SMOVJCMCM
879	9.2	57.5	53	29	BX004390	ArabiDops	C 952	9.2	57.5	64	12	BI912407	BI912407 603290867
880	9.2	57.5	54	9	AU006791	AU006791	C 953	9.2	57.5	64	14	CB277338	CB277338 ku64b09.y

C 954	9.2	57.5	64	28	AZ303997	IM0003K01
C 955	9.2	57.5	64	28	BH417291	1007053G0
C 956	9.2	57.5	64	28	BH857316	SLK_0764
C 957	9.2	57.5	64	29	CNS0080W	AL051183 Drosophila
C 958	9.2	57.5	65	9	AW706445	AW706445 g558e03.y
C 959	9.2	57.5	65	12	BM307132	BM307132 eak37b08.
C 960	9.2	57.5	65	14	CB274956	CB274956 ku73601.y
C 961	9.2	57.5	65	28	BH905328	BH905328 SLK_1059
C 962	9.2	57.5	65	29	BZ764972	BZ764972 SLK_1275
C 963	9.2	57.5	66	9	BX535185	BX535185 Arabidops
C 964	9.2	57.5	66	9	AA904699	AA904699 c374c01.b
C 965	9.2	57.5	66	10	AM394707	AM394707 bh34c12.y
C 966	9.2	57.5	66	10	BG511805	BG511805 nag64g04.
C 967	9.2	57.5	66	12	BG563172	BG563172 602582083
C 968	9.2	57.5	66	12	BM285374	BM285374 EST00013
C 969	9.2	57.5	66	13	BM493230	BM493230 EST00013
C 970	9.2	57.5	66	28	BQ094075	BQ094075 040802.34
C 971	9.2	57.5	66	28	AZ454616	AZ454616 1M0256G08
C 972	9.2	57.5	66	28	AZ587580	AZ587580 1M0395B24
C 973	9.2	57.5	66	28	AZ777009	AZ777009 2M0011B09
C 974	9.2	57.5	66	28	BH214989	BH214989 1006012F0
C 975	9.2	57.5	66	28	BH862885	BH862885 SLK_0907
C 976	9.2	57.5	66	28	BH862895	BH862895 SLK_0907
C 977	9.2	57.5	67	9	AA910136	AA910136 CG04b02.b
C 978	9.2	57.5	67	9	AA916248	AA916248 0155a03.b
C 979	9.2	57.5	67	9	AA159257	AA159257 v288D08.r
C 980	9.2	57.5	67	9	AA159257	AA159257 v288D08.r
C 981	9.2	57.5	67	12	BI782932	BI782932 kd4b11.y
C 982	9.2	57.5	68	9	AI142036	AI142036 ce98b03.x
C 983	9.2	57.5	68	9	AI197097	AI197097 w22c09.x
C 984	9.2	57.5	68	9	AU259479	AU259479 AU259479
C 985	9.2	57.5	68	9	AU266458	AU266458 AU266458
C 986	9.2	57.5	68	10	BF713269	BF713269 MI-P-O2-a
C 987	9.2	57.5	68	11	CNS08M76	CNS08M76
C 988	9.2	57.5	68	14	CB365575	CB365575 ZF001-P00
C 989	9.2	57.5	68	28	BH214675	BH214675 1006004B0
C 990	9.2	57.5	68	29	CC038187	CC038187 3591.1.93
C 991	9.2	57.5	68	29	CC156334	CC156334 KST062.Ba
C 992	9.2	57.5	68	29	AL766655	AL766655 Arabidops
C 993	9.2	57.5	69	9	AI930720	AI930720 bc46a06.y
C 994	9.2	57.5	69	9	AA168290	AA168290 ms22t06.f
C 995	9.2	57.5	69	9	AL796775	AL796775 AL796775
C 996	9.2	57.5	69	10	BG019208	BG019208 daa75E08.
C 997	9.2	57.5	69	12	BJ054370	BJ054370
C 998	9.2	57.5	69	28	AZ419344	AZ419344 1M0195L14
C 999	9.2	57.5	69	28	AZ497061	AZ497061 1M0333F14
C 1000	9.2	57.5	69	28	AZ605602	AZ605602 1M0427G05

## ALIGNMENTS

RESULT 1  
CA798147 80 bp mRNA linear EST 05-DEC-2002  
LOCUS Cac\_BL\_5432 Cac\_BL (Bean and leaf from Amelonardo type Cacao)  
DEFINITION Theobroma cacao cDNA clone Cac\_BL\_5432 5', mRNA sequence.  
ACCESSION CA798147  
VERSION CA798147.1 GI:26055233  
KEYWORDS EST.  
SOURCE Theobroma cacao (cacao)  
ORGANISM Theobroma cacao  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Malvales; Malvaceae; Byttnerioideae; Theobroma.  
REFERENCE Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel, E.R. and Jones, C.A.  
AUTHORS Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel, E.R. and Jones, C.A.  
TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties  
JOURNAL Plantia 216 (2), 255-264 (2002)  
MEDLINE 22337596  
PUBMED 12447539

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Email: Paul.Jones@eu.affem.com  
Seq primer: 73.  
FEATURES  
source  
Location/Qualifiers  
1..80  
/organism="Theobroma cacao"  
/mol\_type="mRNA"  
/strain="Amelonardo type"  
/db\_xref="taxon:3641"  
/clone="Cac BL 5432"  
/tissue\_type="Mature leaf and mature bean"  
/cell\_type="Whole organ"  
/dev\_stage="maturity"  
/lab\_host="XL-1 Blue MRP"  
/clone\_id="Cac\_BL (Bean and leaf from Amelonardo type Cacao)"  
/note="Vector: pBK-CMV; Bean and leaf tissue from an Amelonardo type Cacao tree."  
BASE COUNT 15 a 17 c 27 g 18 t 3 others  
ORIGIN  
Query Match 81.2%; Score 13; DB 14; Length 80;  
Best Local Similarity 86.7%; Pred. No. 5.9e+03;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RGGCTAGTCAACG 15  
:|||||||  
DB 36 GGGCTAGTCAACG 50  
RESULT 2  
A2658330 100 bp DNA linear GSS 14-DEC-2000  
LOCUS A2658330  
DEFINITION IM0535M02F Mouse 10kb plasmid UDCIM library Mus musculus genomic clone UDCIM0535M02 F, genomic survey sequence.  
ACCESSION A2658330  
VERSION A2658330.1 GI:11795476  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D. Weis, R.  
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0535 row: M column: 02  
Seq primer: CGGTGAAACACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 100.  
FEATURES  
source  
Location/Qualifiers  
1..100  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UDCIM0535M02"

```

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnarses/). The DNA
was hydrodynamically sheared by repeated passages through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      23 a      13 c      36 g      28 t
ORIGIN

Query Match      78.8%; Score 12.6; DB 28; Length 100;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 1; Mismatches 0; Gaps 0;
Indels 0;

Cy 1 RGGCTAGCTACAA 13
   :|||||
   5 GGGCTAGCTACAA 17

RESULT 3
BG422154/c
LOCUS      44 bp      mRNA      linear      EST 14-MAR-2001
DEFINITION 602448881P1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4587189 5',
            mRNA sequence.
ACCESSION  BG422154
VERSION     BG422154.1 GI:13328660
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 44)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgsab@xmail.nih.gov
            Tissue Procurement: DCTD/DRP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LMN at:
            http://image.llnl.gov
            Plate: L1CM1317 row: b column: 22
            High quality sequence stop: 44.
            Location/Qualifiers
                1..44
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4587189"
                /tissue_type="renal cell adenocarcinoma"
                /lab host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_14"
                /note="Organ: kidney; Vector: POT87; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'

```

```

adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA Synthesis Kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT      6 a      10 c      21 g      7 t
ORIGIN

Query Match      77.5%; Score 12.4; DB 10; Length 44;
Best Local Similarity 81.2%; Pred. No. 1e+04;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 RGGCTAGCTACAA 16
   :|||||
   39 AGGCACGCTACGCGA 24

RESULT 4
BH901408/c
LOCUS      26 bp      DNA      linear      GSS 04-SEP-2002
DEFINITION SAUK_079024.36.15.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SAUK_079024.36.15.x, genomic
            survey sequence.
ACCESSION  BH901408.1 GI:22712289
VERSION     BH901408
KEYWORDS   GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 26)
            Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predhals,L., Shinn,P.,
            Zimmerman,J., and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
                1..26
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="SAUK_079024.36.15.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT      6 a      6 c      3 g      11 t
ORIGIN

Query Match      75.0%; Score 12; DB 28; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 GGCTAGCTACAA 13
   :|||||
   21 GGCTAGCTACAA 10

```

RESULT 5  
 BUB66082 75 bp mRNA linear EST 16-OCT-2002  
 LOCUS BUB66082/c  
 DEFINITION S062801 Populus imbed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.  
 ACCESSION BUB66082  
 VERSION BUB66082.1 GI:24056736  
 KEYWORDS EST.  
 SOURCE Populus tremula x Populus tremuloides  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Malpighiales; Salicaceae; Populus.  
 1 (bases 1 to 75)  
 Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 JOURNAL Unpublished  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.  
 Location/Qualifiers  
 1..75  
 /organism="Populus tremula x Populus tremuloides"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:47664"  
 /tissue\_type="imbed seed"  
 /clone\_lib="Populus imbed seed cDNA library"  
 20 c 12 g 20 t

BASE COUNT 23 a 20 c 12 g 20 t

ORIGIN

Query Match 75.0%; Score 12; DB 13; Length 75;  
 Best Local Similarity 85.7%; Pred. No. 2.1e+04;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAC 14  
 : |||||  
 54 AGGCTAGCTAGAAC 41

RESULT 6  
 BUB67160 95 bp mRNA linear EST 16-OCT-2002  
 LOCUS BUB67160/c  
 DEFINITION S075A07 Populus imbed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.  
 ACCESSION BUB67160  
 VERSION BUB67160.1 GI:24057814  
 KEYWORDS EST.  
 SOURCE Populus tremula x Populus tremuloides  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Malpighiales; Salicaceae; Populus.  
 1 (bases 1 to 95)  
 Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 JOURNAL Unpublished  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.  
 Location/Qualifiers  
 1..95  
 /organism="Populus tremula x Populus tremuloides"

FEATURES  
 source

RESULT 7  
 BUB62306 96 bp mRNA linear EST 16-OCT-2002  
 LOCUS BUB62306/c  
 DEFINITION S014A04 Populus imbed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.  
 ACCESSION BUB62306  
 VERSION BUB62306.1 GI:24048366  
 KEYWORDS EST.  
 SOURCE Populus tremula x Populus tremuloides  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Malpighiales; Salicaceae; Populus.  
 1 (bases 1 to 96)  
 Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 JOURNAL Unpublished  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.  
 Location/Qualifiers  
 1..96  
 /organism="Populus tremula x Populus tremuloides"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:47664"  
 /tissue\_type="imbed seed"  
 /clone\_lib="Populus imbed seed cDNA library"  
 27 a 27 c 16 g 26 t

BASE COUNT 27 a 27 c 16 g 26 t

ORIGIN

Query Match 75.0%; Score 12; DB 13; Length 96;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+04;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAC 14  
 : |||||  
 46 AGGCTAGCTAGAAC 33

RESULT 8  
 BUB61867 100 bp mRNA linear EST 16-OCT-2002  
 LOCUS BUB61867/c  
 DEFINITION S007G10 Populus imbed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.  
 ACCESSION BUB61867  
 VERSION BUB61867.1 GI:24047927  
 KEYWORDS EST.  
 SOURCE Populus tremula x Populus tremuloides  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Malpighiales; Salicaceae; Populus.  
 1 (bases 1 to 100)  
 Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 JOURNAL Unpublished  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.  
 Location/Qualifiers  
 1..100  
 /organism="Populus tremula x Populus tremuloides"

FEATURES  
 source

REFERENCE 1 (bases 1 to 100)  
 AUTHORS Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags  
 from multiple libraries  
 JOURNAL Unpublished  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.  
 Location/Qualifiers  
 1..100  
 /organism="Populus tremula x Populus tremuloides"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:47664"  
 /tissue\_type="imbibed seed"  
 /clone\_lib="Populus imbibed seed cDNA library"  
 BASE COUNT 22 a 25 c 20 g 29 t  
 ORIGIN

Query Match 75.0%; Score 12; DB 13; Length 100;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+04;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RGCTAGCTACAC 14  
 :|||||||  
 Db 37 AGGCTAGCTAGAC 24

RESULT 9  
 A2619815/c 80 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0452D18F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 DEFINITION clone UGCG1M0452D18 F, genomic survey sequence.  
 A2619815  
 A2619815.1 GI:11742005  
 GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 80)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished  
 JOURNAL Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0452 row: D column: 18  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 80.  
 Location/Qualifiers  
 1..80  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="CS7BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCG1M0452D18"  
 /sex="Male"  
 /lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: pMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g14732114[gb|AF129072.1]) a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 20 a 15 c 21 g 24 t  
 ORIGIN

Query Match 72.5%; Score 11.6; DB 28; Length 80;  
 Best Local Similarity 91.7%; Pred. No. 3.5e+04;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACA 12  
 :|||||||  
 Db 28 AGGCTAGCTACA 17

RESULT 10  
 H08942 52 bp mRNA linear EST 23-JUN-1995  
 LOCUS Y13605.r1 Soares infant brain INB Homo sapiens cDNA clone  
 DEFINITION IMAGE:45750 5', similar to gb|M87909|HUMANLN36 Human carcinoma  
 cell-derived Alu RNA transcript, (rRNA); gb:M2315 TUMOR NECROSIS  
 FACTOR RECEPTOR 2 PRECURSOR (HUMAN), mRNA sequence.  
 H08942  
 H08942.1 GI:873764  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 52)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,  
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaekis, E., Waterston,  
 R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The Washu-Merck EST Project  
 Unpublished  
 JOURNAL Contact: Wilson RK  
 Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1449  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LNLN  
 This clone is available royalty-free through LNLN; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert Length: 1449 Std Error: 0.00  
 Seq primer: M13RPI  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..52  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

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/db_xref="GDB:418291"
/db_xref="taxon:9606"
/clone="IMAGB:45750"
/sex="female"
/dev stage="73 days post natal"
/lab host="DH10B (ampicillin resistant)"
/clone_1b="Soares infant brain INTB"
/notes:Organ: Whole Brain; Vector: Latmid BA; Site 1: Not
1; Site 2: Hind III; 1st strand cDNA was primed with a Not
1 - oligo (dt) primer 15'
AACTGAGAGATTGCGCGCAGCAATTTTTTTTTTTTTTTT 3';
double-stranded cDNA was ligated to Hind III adaptors
(pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Latmid BA vector.
Library went through one round of normalisation. Library
constructed by Bento Soares and M.Patima Bonaldo."
BASE COUNT      8 a      16 c      11 g      11 t      6 others
ORIGIN

Query Match      71.2%; Score 11.4; DB 14; Length 52;
Best Local Similarity 92.3%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 GGCTAGCTACAC 14
      |||||
      30 GGCTGCTACAC 42

RESULT 11
N98196      74 bp mRNA linear EST 18-NOV-1996
LOCUS      0266C3 czappdpd2.1, Debopam Chakrabarti Plasmodium falciparum cDNA
DEFINITION clone PF0266C, mRNA sequence.
ACCESSION  N98196
VERSION     N98196
KEYWORDS   EST.
SOURCE     Plasmodium falciparum (malaria parasite P. falciparum)
ORGANISM   Plasmodium falciparum
REFERENCE  1 (bases 1 to 74)
AUTHORS   Dame,J.B., Arnot,D.E., Bouke,P., Chakrabarti,D., Christodoulou,Z.,
Coppel,R., Cowman,A., Craig,A., Fischer,K., Foster,J., Goodman,N.,
Hinterberg,K., Holder,A.A., Holt,D., Kemp,D., Lanzer,M., Lim,A.,
Newbold,C., Ravetch,J.V., Reddy,G.R., Rubio,J., Schuster,S.M., Su
,X.-Z., Thompson,J.K., Vitali,F., Williams,T.B. and Werner,E.
TITLE     Current status of the Plasmodium falciparum genome project
JOURNAL   Mol. Biochem. Parasitol. 79, 1-12 (1996)
MEDLINE   97001675
PUBMED    8844667
COMMENT   Contact: Debopam Chakrabarti
           Department of Molecular Biology and Microbiology
           University of Central Florida
           Orlando, FL 32816-2360
           Tel: 407 384 2061
           Fax: 407 384 3095
           Email: dchak@pegasus.cc.ucf.edu
           Seq primer: 73
           Location/Qualifiers
             1..74
               /organism="Plasmodium falciparum"
               /mol_type="mRNA"
               /strain="Dd2"
               /db_xref="taxon:5833"
               /clone="PF0266C"
               /lab host="E. coli XL-1 blue"
               /note="Vector: lambda ZAP II; Site 1: Ecor I; Site 2: Xho
               I; PolyA+ RNA, from asynchronous blood stage parasites of
               the Dd2 isolate cultured in vitro, was reverse transcribed
               using an oligo dt-Xho I primer. Second strand was
               prepared using RNase H and DNA polymerase I. Ecor I
               adapters were ligated to the cDNA, and it was digested
               with Xho I. Prepared fragments were ligated into Ecor I +

```

```

Xho I digested lambda ZAP II vector. "
BASE COUNT      18 a      17 c      12 g      14 t      13 others
ORIGIN

Query Match      71.2%; Score 11.4; DB 14; Length 74;
Best Local Similarity 85.7%; Pred. No. 4.4e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      3 GCTAGCTACACGA 16
      |||||
      43 GCTAGCTACACGA 56

RESULT 12
BX535085      76 bp DNA linear GSS 03-JUN-2003
LOCUS      Arabidopsis thaliana T-DNA flanking sequence GK-514H05-019924,
DEFINITION genomic survey sequence.
ACCESSION  BX535085
VERSION     BX535085
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1
AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
and Weishaar,B.
TITLE     A pipeline for automated high-throughput generation of FSTs
           (flanking sequence tags) from Arabidopsis thaliana T-DNA
           transformed lines
           Unpublished
REFERENCE  2
AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weishaar,B.
TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
           for flanking sequence tag based reverse genetics
           Unpublished
JOURNAL    Submitted (02-JUN-2003) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
AUTHORS   Li,Y., Strizhov,N., Rosso,M. and Weishaar,B.
TITLE     Direct Submission
JOURNAL    Submitted (02-JUN-2003) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT   This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At3g53040. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpi-z-koeln.mpg.de/GABI-Kat/.
           Location/Qualifiers
             1..76
               /organism="Arabidopsis thaliana"
               /mol_type="genomic DNA"
               /strain="Columbia 0"
               /db_xref="taxon:3702"
               /clone="GK-514H05-019924"
               /note="PCR was performed on DNA from Arabidopsis thaliana
               plants (T1) which were transformed with the T-DNA from
               vector pAC161. The lines contain one or more T-DNA
               insertions. The DNA fragment(s) resulting from the PCR
               were directly sequenced to determine the genomic sequence
               flanking the insertion. Sequences displaying significant
               similarity to the A. thaliana nuclear genome sequence were
               processed for submission. T-DNA derived sequences were
               removed"
BASE COUNT      24 a      19 c      24 g      9 t
ORIGIN

Query Match      71.2%; Score 11.4; DB 29; Length 76;
Best Local Similarity 80.0%; Pred. No. 4.4e+04;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 RGCTAGCTACAAG 15  
 Db 75 AGCTAGCTGAGCG 61

RESULT 13  
 LOCUS A1461140 95 bp mRNA linear EST 28-NOV-2001  
 DEFINITION B675F01.Y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-cl004-5138 5', mRNA sequence.  
 A1461140  
 VERSION A1461140.1 GI:4314021  
 KEYWORDS EST.  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids  
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 95)  
 Shoemaker, R., Keim, P., Vodkin, L., Expelding, J., Coryell, V., Khanna  
 , A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers  
 , Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk  
 , R., Ritter, E., Kohn, S., Shin, T., Jackson, T., Cardenas, M., McCann  
 , R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: east@watson.wustl.edu  
 This clone is available through: Reagen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntville, AL 35801 For further information  
 call: (800)-533-4363 or contact via email: ccu@reagen.com  
 Insert Length: 369 Std Error: 0.00  
 Seq primer: -40RP from Gldco  
 POLYA-No.

FEATURES  
 source  
 1..95  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl004-5138"  
 /issue\_type="root"  
 /lab\_host="XL10-Gold"  
 /clone\_id="Gm-cl004"  
 /note="Vector: pBluescript II Xr; Site 1: EcoRI; Site 2:  
 XhoI; Root cDNA. The mRNA was isolated from entire roots  
 of 8 day old 'Williams' seedlings which were propagated on  
 paper towels with distilled water. Stragene's cDNA  
 synthesis kit (catalog #200401) was used to synthesize the  
 cDNA. First-strand synthesis was performed with 5-methyl  
 dCTP, hence the ligated cDNA is hemimethylated.  
 Stragene's first-strand synthesis primer was used  
 (GAGAGAGAGAGAGAGAGACTGCTGAG(T)-18). After  
 second-strand synthesis, the cDNA ends were 'polished',  
 with clone Pfu DNA polymerase, ligated to EcoRI adapters,  
 and phosphorylated. The XhoI site within the first-strand  
 synthesis primer was restricted by digestion with XhoI;  
 all XhoI sites in the cDNA would be protected by their  
 hemimethylated status. The cDNA constructs were  
 size-fractionated with a 500bp cutoff, using GbhcoRI. Life  
 Technologies' cDNA Size Fractionation column. The column  
 eluent was then ligated into Stragene's pBluescript II  
 XR predigested vector (pBluescript II SK(+)) that had been  
 digested with EcoRI and XhoI, and phosphorylated). Both  
 the white and blue colonies appear to contain recombinant  
 plasmids with cDNA inserts. Blue colonies 9n=15) have been

BASE COUNT  
 ORIGIN 25 a 25 c 18 g 27 t

Query Match 71.2%; Score 11.4; DB 9; Length 95;  
 Best Local Similarity 80.0%; Pred. No. 4.8e+04;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAAG 15  
 Db 52 GGTCCTGCTACAAG 66

RESULT 14  
 LOCUS B0823860/c 95 bp mRNA linear EST 01-AUG-2002  
 DEFINITION 1030113D08.x1 C. reinhardtii CC-1690, Deflagellation (normalized),  
 Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.  
 B0823860  
 VERSION B0823860.1 GI:22075084  
 KEYWORDS EST.  
 SOURCE Chlamydomonas reinhardtii  
 ORGANISM Chlamydomonas reinhardtii  
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 Chlamydomonadales; Chlamydomonas.  
 1 (bases 1 to 95)  
 Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre  
 , P., McDermott, J.P., Shrago, J., Sillflow, C. and Stern, D.  
 Analyses of the Chlamydomonas reinhardtii Genome: A Model,  
 Unicellular System for Analyzing Gene Function and Regulation in  
 Vascular Plants. Project: 1030  
 Unpublished  
 Contact: Charles Hauser  
 DCMB Box 91000  
 Duke University  
 Durham, NC 27708-1000  
 Tel: 919 613 8159  
 Fax: 919 613 8177  
 Email: chause@duke.edu.

FEATURES  
 source  
 1..95  
 /organism="Chlamydomonas reinhardtii"  
 /mol\_type="mRNA"  
 /strain="CC-1690 wild type mt+ 21gr"  
 /db\_xref="taxon:3055"  
 /clone\_id="C. reinhardtii CC-1690, Deflagellation  
 (normalized), Lambda Zap II"  
 /note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:  
 XhoI; Deflagellation library, constructed by John Davies  
 and Jeffrey McDermott, combines cDNAs from CC-1690 cells  
 which had been re-synthesizing flagella for 15, 30 and 60  
 min after being deflagellated by pH shock. PolyA mRNA was  
 purified from each sample, pooled and cDNA synthesized.  
 The cDNA was directionally cloned into lambda Zap II  
 (Stratagene) in the EcoRI (5') and XhoI (3') sites.  
 pBluescript II SK- plasmids were excised from the lambda  
 Zap clones by superinfection with ExAssist (Stratagene)  
 phage. The library was normalized using method 4 described  
 in Bonaldo et al., (1996) Genome Research 6: 791-806."

BASE COUNT  
 ORIGIN 21 a 30 c 14 g 30 t

Query Match 71.2%; Score 11.4; DB 13; Length 95;  
 Best Local Similarity 92.3%; Pred. No. 4.8e+04;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCTAGCTACAAG 15

sequenced, and possess putative cDNA inserts. This library  
 was constructed by Dr. Paul Keim & Virginia H. Coryell,  
 Department of Biology, Box5640, Northern Arizona  
 University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.  
 Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:  
 520-523-7500, email: Paul.Keim@nau.edu,  
 Virginia.coryell@nau.edu"

Db 66 GGTACTACAAACG 54

RESULT 15  
LOCUS AZ916132 96 bp DNA linear GSS 15-MAR-2001  
DEFINITION Pct1.3.a8-c-1.0 Maize Pct1 B73 leaf Zea mays genomic, genomic  
survey sequence.  
ACCESSION AZ916132  
VERSION AZ916132.1 GI:13347408  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 96)  
Missouri Maize Project--Maize Mapping Project.  
Pct1 Zea mays B73 Pct1 leaf tissue library  
Unpublished  
CONTACT: Schroeder S  
Missouri Maize Project--Maize Mapping Project  
University of Missouri  
209 Curtis Hall, Columbia, MO 65211, USA  
Tel: 573 882 8214  
Fax: 573 884 7850  
Email: sschroeder@celephais.agron.missouri.edu  
Class: shotgun.

FEATURES  
source  
1..96  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/lab\_host="DHS alpha"  
/clone\_lib="Maize Pct1 B73 leaf"  
/note="Organ: Leaf; Vector: PUC19; Pct1 digested B73  
genomic sucrose gradient size fractionated fragment sizes  
of 0.5kb to 2kb ligated to PUC19 transformed in DHS alpha"

BASE COUNT 22 a 29 c 27 g 18 t

ORIGIN

Query Match 71.2%; Score 11.4; DB 28; Length 96;  
Best Local Similarity 80.0%; Pred. No. 4.8e+04;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 1 RGGCTAGCTACAAACG 15  
DB 80 AGCTTAGCTACAAATG 94

RESULT 16  
LOCUS BX288422 58 bp DNA linear GSS 07-MAR-2003  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-414B10-018037,  
genomic survey sequence.  
ACCESSION BX288422  
VERSION BX288422.1 GI:28887418  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1  
Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Siedler,H.  
and Weishaar,B.  
A pipeline for automated high-throughput generation of ESTs  
(flanking sequence tags) from Arabidopsis thaliana T-DNA  
transformed lines  
Unpublished

REFERENCE 2  
AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weishaar,B.  
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
for flanking sequence tag based reverse genetics  
JOURNAL Unpublished  
AUTHORS Strizhov,N., Rosso,M., Li,Y. and Weishaar,B.  
TITLE 3 (bases 1 to 58)  
JOURNAL Direct Submission  
COMMENT Submitted (07-MAR-2003) Weishaar B., Max-Planck-Institut fuer  
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence is recovered from the left border of the T-DNA. It  
indicates an insertion close to or within gene At3g53810. The  
sequences are generated at the MPI for Plant Breeding Research in  
the context of the GABI-Kat project. GABI-Kat is part of the German  
Plant Genomics program designated 'GABI'. Information on line  
availability can be found at:  
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES  
source  
1..58  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-414B10-018037"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/note="PCR was performed on DNA from Arabidopsis thaliana  
plants (T1) which were transformed with the T-DNA from  
vector pAC161. The lines contain one or more T-DNA  
insertions. The DNA fragment(s) resulting from the PCR  
were directly sequenced to determine the genomic sequence  
flanking the insertion. Sequences displaying significant  
similarity to the A. thaliana nuclear genome sequence were  
processed for submission. T-DNA derived sequences were  
removed"

BASE COUNT 15 a 17 c 11 g 15 t

ORIGIN

Query Match 68.8%; Score 11; DB 29; Length 58;  
Best Local Similarity 100.0%; Pred. No. 6.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 AGCTACAAACA 16  
DB 49 AGCTACAAACA 39

RESULT 17  
LOCUS H62825 73 bp mRNA linear EST 10-OCT-1995  
DEFINITION y746e04.s1 Soares fetal liver spleen INFIS Homo sapiens cDNA clone  
IMAGE:208350 3' similar to gb:M22918 MYOSIN LIGHT CHAIN ALKALI,  
SMOOTH-MUSCLE ISOFORM (HUMAN);, mRNA sequence.  
ACCESSION H62825  
VERSION H62825.1 GI:1017171  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 73)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
'M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maira,M., Parsons,D.,  
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston  
R., Williamson,A., Wohlmann,P. and Wilson,R.  
The WashU-Merck EST Project  
Unpublished  
CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Insert Size: 705

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: zbratish@watson.wustl.edu  
cDNA Library constructed by S. Linn DNA Sequencing by: Washington  
University Genome Sequencing Center Clone distribution: the  
I.M.A.G.E. Consortium/BLNI, send email to: info@image.llnl.gov  
seq primer: T7 from Gibco.

lab host="E. coli strain XL10-Gold, T1-resistant, F<sup>-</sup>/clone.lib="Mouse 10kb plasmid UGCC2M library"/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 20 a 21 c 21 g 22 t  
ORIGIN

Query Match 68.8%; Score 11; DB 28; Length 84;  
Best Local Similarity 84.6%; Pred. No. 7.6e+04;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCGTACTACAA 13  
:|||||  
Db 59 AGGCTGCTACAA 71

RESULT 20 90 bp mRNA linear EST 08-MAR-2000  
AI937714  
LOCUS wp89a12.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2468350 3'  
DEFINITION similar to gb:K63563 DNA-DIRECTED RNA POLYMERASE II 140 KD  
POLYPEPTIDE (HUMAN); mRNA sequence.  
AI937714  
AI937714.1 GI:5676584  
EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90)  
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index

Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 764 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
SOURCE

1..90  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="2468350"  
/tissue\_image="anaplastic oligodendroglioma"  
/lab\_host="DH10B"  
/clone\_1lb="NCI CGAP Brn25"  
/note="Organ: brain; Vector: pRTT3D-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTCACCAATCTAGAGGAGCGCCGACATGTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pRTT3 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 25 a 10 c 16 g 39 t  
ORIGIN

Query Match 68.8%; Score 11; DB 9; Length 90;  
Best Local Similarity 84.6%; Pred. No. 7.8e+04;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCGTACTACAA 13  
:|||||  
Db 81 AGGCTACTACAA 69

RESULT 21 90 bp DNA linear GSS 05-AUG-2002  
BH861753  
LOCUS SALK\_087935 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
DEFINITION thaliana genomic clone SALK\_087935, genomic survey sequence.  
BH861753  
VERSION BH861753.1 GI:22097079  
KEYWORDS  
SOURCE  
ORGANISM

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE

1 (bases 1 to 90)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel.: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: [ecker@salk.edu](mailto:ecker@salk.edu)

This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated exon of At2g27170.  
Class: TDNA tagged.  
Location/Qualifiers

FEATURES  
SOURCE

1..90  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_1lb="SALK\_087935"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

BASE COUNT 34 a 17 c 14 g 25 t  
ORIGIN

Query Match 68.8%; Score 11; DB 28; Length 90;  
Best Local Similarity 84.6%; Pred. No. 7.8e+04;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCGTACTACAA 13  
:|||||  
Db 41 AGGCTACTACAA 53

RESULT 22  
AG224693 91 bp DNA linear GSS 12-DEC-2002  
LOCUS Ag224693  
DEFINITION Locus japonicus DNA, clone:UjB1a20\_f, genomic survey sequence.  
ACCESSION AG224693  
VERSION AG224693.1 GI:26534755  
KEYWORDS GSS.  
SOURCE Locus japonicus  
ORGANISM Locus japonicus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae; Locus.

REFERENCE 1  
Sato, S., Nakamura, Y. and Tabata, S.  
TITLE Locus japonicus BAC End sequences  
JOURNAL Published Only in Database (2002)  
REFERENCE 2 (bases 1 to 91)  
AUTHORS Sato, S.  
TITLE Direct Submission  
JOURNAL Submitted (20-NOV-2002) Shusui Sato, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; 2-6-7  
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan  
(E-mail: sato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/, Tel: 81-438-52-3935 (ex.2336), Fax: 81-438-52-3934)  
LOCATION/Qualifiers

FEATURES  
source  
1..91  
/organism="Locus japonicus"  
/mol\_type="genomic DNA"  
/strain="Miyakojima MG-20"  
/db\_xref="taxon:34305"  
/clone="UjB1a20\_f"  
/clone\_1ib="genomic BAC library"  
/note="VECTOR: pBE10BAC11"

BASE COUNT 26 a 23 c 18 g 24 t  
ORIGIN

Query Match 68.8%; Score 11; DB 29; Length 91;  
Best Local Similarity 100.0%; Pred. No. 7.8e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTAGCTACAC 14  
|||||  
62 CTAGCTACAC 72

Db

RESULT 23  
AZ431360 96 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M021614F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M021614 F, genomic survey sequence.  
ACCESSION AZ431360  
VERSION AZ431360.1 GI:10555373  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 96)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
CONTACT Contact: Robert B. Weiss  
UNIVERSITY University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddumgenetics@utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0216 row: F column: 14  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 96.

FEATURES  
source  
1..96  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M021614"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 31 a 32 c 12 g 21 t  
ORIGIN

Query Match 68.8%; Score 11; DB 28; Length 96;  
Best Local Similarity 84.6%; Pred. No. 8e+04;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAA 13  
:|||||  
4 GGCTAGCCACAA 16

Db

RESULT 24  
A1681141 49 bp mRNA linear EST 26-MAY-1999  
LOCUS tx44007.x1 NCI CGAP Lu24 Homo sapiens cDNA IMAGE:227429.3  
DEFINITION similar to SW:R33A HUMAN P54725 UV EXCISION REPAIR PROTEIN  
ACCESSION RAD23 HOMOLOG A, mRNA sequence.  
VERSION A1681141  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 49)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished  
CONTACT Contact: Robert Straubeberg, Ph.D.  
EMAIL Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILMIL at:  
 www.bio.lnlnl.gov/bdrip/image/image.html

Trace considered overall poor quality  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers

FEATURES  
 source  
 1. 49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2272429"  
 /issue\_type="carchinoid"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Lu24"  
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI-CGAP\_Lus was prepared, and as circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (clones  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT  
 ORIGIN  
 Query Match 67.5%; Score 10.8; DB 9; Length 49;  
 Best Local Similarity 85.7%; Pred. No. 8e+04; 2; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GCTAGCTACACGA 16  
 |||||  
 29 GCCAGCTACACAA 42

RESULT 25  
 AUI06358/c 50 bp mRNA linear EST 30-AUG-2001  
 LOCUS AUI06358 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION HEPO2980, mRNA sequence.  
 ACCESSION AUI06358  
 VERSION AUI06358  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
 'H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
 'Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)  
 21270072  
 11375929

COMMENT  
 Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
 'S. Construction and characterization of a full length-enriched and  
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
 source  
 1. 50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HEPO2980"

BASE COUNT  
 ORIGIN  
 /clone\_lib="Sugano Homo sapiens cDNA library"  
 3 a 20 c 12 g 15 t

Query Match 67.5%; Score 10.8; DB 9; Length 50;  
 Best Local Similarity 85.7%; Pred. No. 8e+04; 2; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GCTAGCTACACGA 16  
 |||||  
 Db 31 GCCAGCTACACAA 18

RESULT 26  
 AA425092 52 bp mRNA linear EST 16-OCT-1997  
 LOCUS AA425092  
 DEFINITION zwilfil.r1 Soares NHPu.S1 Homo sapiens cDNA clone IMAGE:769005.5,  
 similar to SW.HESI\_MOUSE P35428 TRANSCRIPTION FACTOR HES-1., mRNA  
 sequence.

ACCESSION AA425092 GI:2107543  
 VERSION AA425092.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 52)  
 Haller, J., Allen, M., Bowles, L., Dubnue, T., Geisel, G., Jost, S.,  
 Kucaba, T., Lacy, M., Le, N., Lemon, G., Marra, M., Martin, J., Moore, B.,  
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie  
 'T., Waterston, R. and Wilson, R.  
 Washu-Merck EST Project 1997  
 Unpublished

REFERENCE  
 AUTHORS

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Wilson R.  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through ILMIL; contact the  
 IMAGE Consortium (info@image.lnlnl.gov) for further information.  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

FEATURES  
 source

1. 52  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:5975323"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:769005"  
 /issue\_type="Pooled human melanocyte, fetal heart, and  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares NHPu.S1"  
 /note="Organ: mixed (see below); Vector: pT73D-Pac  
 (Pharmacia) with a modified polylinker; Site 1: Not I;  
 Site 2: Eco RI; Equal amounts of plasmid DNA from three  
 normalized libraries (melanocyte 2NHPu, pregnant uterus  
 NHPu, and fetal heart NHPu) were mixed, and as circles  
 were used as tracer in a subtractive hybridization,  
 reaction. The driver was PCR-amplified cDNAs from pools of  
 5,000 clones made from the same 3 libraries. The pools  
 consisted of I.M.A.G.E. clones 260232-265223,  
 340488-345479, and 484488-489479."

BASE COUNT  
 ORIGIN  
 Query Match 67.5%; Score 10.8; DB 9; Length 52;  
 Best Local Similarity 85.7%; Pred. No. 8.2e+04; 2; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

0y	3	GCTAGCTCAACGA	16		
Db	38	GCACGCTTCAACGA	51		
RESULT 27					
LOCUS	B2765391				
DEFINITION	B2765391	52 bp	DNA	linear	GEN 13-MAR-2003
ACCESSION	B2765391				
VERSION	B2765391				
KEYWORDS	B2765391				
SOURCE	B2765391.1	GI:28937944			
ORGANISM	Arabidopsis thaliana (chale cress)				
REFERENCE	Arabidopsis thaliana				
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
TITLE	Alonso,J.M., Leisner,T.J., Barjae,P., Chen,H., Chouk,R., Gadriab,C., Jeeke,A., Karnes,M., Kim,C.V., Parker,H., Prednis,L., Shinn,P., Zimmermann,J., and Ecker,J.R.				
JOURNAL	A sequence-indexed library of insertion mutations in the Arabidopsis Genome				
COMMENT	Unpublished				
CONTACT	Contact: Joseph R. Ecker				
LOCUS	Salk Institute Genomic Analysis Laboratory (SIGAL)				
DEFINITION	The Salk Institute for Biological Studies				
KEYWORDS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA				
SOURCE	Tel: 858 453 4100 x1752				
ORGANISM	Fax: 858 558 6379				
REFERENCE	Email: ecker@salk.edu				
AUTHORS	This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At4g38910.				
TITLE	Class: TDNA tagged.				
JOURNAL	Location/Qualifiers				
COMMENT	1..52				
LOCUS	/organism="Arabidopsis thaliana"				
DEFINITION	/mol_type="genomic DNA"				
KEYWORDS	/strain="Columbia 0"				
SOURCE	/db_xref="taxon:3702"				
ORGANISM	/clone="SALK_131129.40.10.x"				
REFERENCE	/note="PCR was performed on Arabidopsis thaliana lines				
AUTHORS	/clone.lib="Arabidopsis thaliana TDNA insertion lines"				
TITLE	each of which contains one or more TDNA insertion				
JOURNAL	elements. The resultant fragment for each line was				
COMMENT	directly sequenced to determine the genomic sequence at				
LOCUS	the site of insertion. Details of the protocols used can				
DEFINITION	be found at <a href="http://signal.salk.edu/tDNA_protocols.html">http://signal.salk.edu/tDNA_protocols.html</a> "				
ACCESSION	16 a	11 c	8 g	17 t	
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
CONTACT					
LOCUS					
DEFINITION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
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DEFINITION					
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COMMENT					
CONTACT					
LOCUS					
DEFINITION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					

	ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE	AUTHORS	Marra,M., Hallier,J., Allen,M., Bowles,M., Dietrich,N., Dubnue,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  The WashU-HHMI Mouse EST Project  Unpublished Contact: Marra M/Mouse Est Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNC ; contact the IMAGE Consortium ( <a href="#">info@image.lnl.gov</a> ) for further information. MGJ:484606
FEATURES	SOURCE	Trace considered overall poor quality Sequence reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 Et from Amersham High quality sequence stop: 1.  Location/Qualifiers 1..58 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /_clone="IMAGE:808262" /_sex="male" /_issue_type="heart" /_dev_stage="4 weeks" /_lab_host="DH10B" /_clone_lib="Soares mouse NBMH" /poly_vector="prT7SD-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dAT) primer [5, TGTTACCATCTGTAAGCGGGCCGCACAATTGTTCCTTTTTTTTTTTTTT (3')]; double-stranded cDNA was ligated to Eco RI adaptors (pharmac), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT		16 a      18 C      4 G      20 t
ORIGIN		
Query Match		67.5%; Score 10.8; DB 9; Length 58;
Best Local Similarity		85.7% Pred. No. 8.5e+04;
Matches	12; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy		3 GC TAG CT ACA CGA 16
Db		16 GA T GG CTC A CA CGA 3
RESULT 29		
AZ342599/c		59 bp DNA linear GSS 29-SEP-2000
LOCUS		1M0075ClR Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION		clone UUCGM0075ClR R, genomic survey sequence.
ACCESSION		AZ342599
VERSION		AZ342599.1 GI:10419997
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	Dunn,D., Ayvagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,	

**TITLE**  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL**  
Unpublished  
**COMMENT**  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0075 Row: C Column: 18  
Seq primer: CACACAGGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 59.  
Location/Qualifiers

**FEATURES**  
source  
1..59  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC1M0075C18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1id="Mouse 10kb plasmid UGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**BASE COUNT**  
11 a 9 c 12 g 27 t

**ORIGIN**  
Query Match 67.5%; Score 10.8; DB 28; Length 59;  
Best Local Similarity 75.0%; Pred. No. 8.6e+04;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

**QY**  
1 RGCGTACCTACACGA 16  
|||  
Db 35 AGGATAGCTAAACAA 20  
  
**RESULT 30**  
CNS06E2T 60 bp DNA linear GSS 17-JUN-2001  
LOCUS T3 end of clone AROAA018A08 of library AROAA from strain CBS 732 of  
DEFINITION Zygocacharomyces rouxii, genomic survey sequence.  
ACCESSION AL394587  
VERSION AL394587.1 GI:12145628  
KEYWORDS GSS.  
ORGANISM Zygocacharomyces rouxii  
SOURCE Zygocacharomyces rouxii  
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
REFERENCE 1 (bases 1 to 60)

**AUTHORS**

Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Boloitchi-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de Montigny, J., Dujon, B., Durieux, P., Leplinge, A., Llorente, B., Malpertuy, A., Neugeilise, C., Ozier-Kalogiropoulos, O., Potier, S., Sarrin, M., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, E., and Weissenbach, J.  
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies  
Yeast Lett. 487 (1), 3-12 (2000)

**JOURNAL**

2 (bases 1 to 60)  
de Montigny, J., Straub, M., Potier, S., Tekala, F., Dujon, B., Wincker, F., Artiguenave, F., and Souciet, J.  
Genomic exploration of the hemiascomycetous yeasts: 8.  
Zygocacharomyces rouxii  
YEAS Lett. 487 (1), 52-55 (2000)

**MEDLINE**

20584718  
1152863  
3 (bases 1 to 60)

**REFERENCE**

Genoscope.  
Direct Submission  
Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)

**COMMENT**

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces kluyveri, Saccharomyces servazii, Zygocacharomyces rouxii, exiguus, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces fragilis, Kluyveromyces marxianus var. marxianus, Pichia lactis var. lactis, Kluyveromyces fragilis var. fragilis, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.  
Location/Qualifiers

**FEATURES**

source  
1..60  
/organism="Zygocacharomyces rouxii"  
/mol\_type="genomic DNA"  
/strain="CBS 732"  
/db\_xref="taxon:4956"  
/clone="AROAA018A08"  
/note="Tend : T3"  
/note="Tend : T3"

**BASE COUNT**

17 a 25 c 11 g 6 t 1 others

**ORIGIN**  
Query Match 67.5%; Score 10.8; DB 29; Length 60;  
Best Local Similarity 80.0%; Pred. No. 8.6e+04;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY**  
2 GGCTAGCTACACGA 16  
|||  
Db 7 GGCTAGCTACACGA 21  
  
**RESULT 31**  
AA070413 61 bp mRNA linear EST 23-DEC-1997  
LOCUS zme8c11.r1 Strata gene neuroepithelium (#937231) Homo sapiens cDNA  
DEFINITION Clone IMAGE:530804 5' similar to SW:ATP6\_MOUSE P00848 ATP SYNTHASE  
A CHAIN : mRNA sequence.  
ACCESSION AA070413  
VERSION AA070413.1 GI:1577774  
KEYWORDS EST.  
ORGANISM Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
KEYWORDS Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 61)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chitapelli, B., Chisoso, S., Dierich, N., Dubuque, T., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore



Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATCGCGACGAG 3' -3' adaptor sequence: 5' CTCGACGTTTTTTTTTTTTTTT 3' "

## BASE COUNT

22 a 5 c 18 g 20 t

## ORIGIN

Query Match 67.5%; Score 10.8; DB 9; Length 65;  
Best Local Similarity 85.7%; Pred. No. 8.9e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GCGTACTACACGA 16

19 GATGCTACACGA 32

## Db

RESULT 34  
BH414369/c 65 bp DNA linear GSS 12-DEC-2001  
LOCUS 1007037602.2EL.X1 1007 - Rescuemu Grid H Zea mays genomic, genomic  
DEFINITION survey sequence.

ACCSSION BH414369.1 GI:17592332

## KEYWORDS

## SOURCE

## ORGANISM

Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 65)

REFERENCE  
Walbot, V.  
Maize genomic sequences found using engineered Rescuemu transposon

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished  
Contact: Walbot, V.  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221

Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1007037 column: 16  
Class: transposon-tagged.

FEATURES  
Location/Qualifiers

1..65

/organism="Zea mays"  
/mol\_type="genomic DNA"  
/culti\_val="mixed background W23/A188/B73"

/db\_xref="taxon:4577"  
/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_11b="1007 - Rescuemu Grid H"

/note="Organ: leaf; Vector: Rescuemu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
Rescuemu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription web  
units. For more information on Rescuemu, go to the  
site 'www.zmh.iasrate.edu' and follow the links for  
'Rescuemu'. Grid H was grown at Berkeley in 2001. DNA  
was extracted from leaf punches, double digested using  
BamHI and BglII, and ligated to form circular plasmids.  
DH10B cells were transformed and then screened on LB  
plates with ampicillin."

## BASE COUNT

11 a 15 c 26 g 13 t

## ORIGIN

Query Match 67.5%; Score 10.8; DB 28; Length 65;  
Best Local Similarity 75.0%; Pred. No. 8.9e+04;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 RGGCTAGCTACACGA 16

Db 17 GGCCACGCTACACGA 2

RESULT 35  
TA184A080/c

LOCUS 65 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 184a08, reverse sequence,  
genomic survey sequence.

ACCSSION AL473539.1 GI:11840567

## KEYWORDS

## SOURCE

## ORGANISM

Trypanosoma brucei  
Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

1 (bases 1 to 65)

REFERENCE  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/

## FEATURES

## source

## Location/Qualifiers

## 1..65

/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"

/db\_xref="taxon:5691"

/clone="184a08"

## BASE COUNT

15 a 11 c 28 t

## ORIGIN

Query Match 67.5%; Score 10.8; DB 29; Length 65;  
Best Local Similarity 75.0%; Pred. No. 8.9e+04;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 RGGCTAGCTACACGA 16

63 GGCCACGCTACACGA 48

## Db

RESULT 36  
BG447495  
LOCUS 66 bp mRNA linear EST 15-MAR-2001  
DEFINITION EST0000018 Rat Liver Express Library Rattus norvegicus cDNA clone  
11ver000018, mRNA sequence.

ACCSSION BG447495.1 GI:13357147

VERSION BG447495.1

KEYWORDS  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

1 (bases 1 to 66)

REFERENCE  
Li, Y.C., Xu, C.S. and Zh, Y.H.

Cloning the specific expressed genes in partial hepatectomy rat  
liver by suppression subtractive hybridization

1 RGGCTAGCTACACGA 16

JOURNAL  
COMMENT Unpublished  
Contact: YC Li  
Department of Biology  
Henan Normal University  
Jianshe road, Xinxiang, China  
Email: lychang@mail.hennu.edu.cn.  
Location/Qualifiers

FEATURES  
SOURCE  
1. .66  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="liver000018"  
/sex="male"  
/tissue\_type="liver"  
/dev\_stage="embryonic day 17 post-fertilization"  
/clone\_lib="Rat Liver Express Library"

BASE COUNT  
ORIGIN  
18 a 17 c 15 g 16 t

Query Match  
Best Local Similarity 67.5%; Score 10.8; DB 10; Length 66;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY  
1 RGCTAGCTACACGA 16  
:|||||  
61 AGGCTGCTCAACA 46

Db  
61 AGGCTGCTCAACA 46

RESULT 37  
AA771119/c 67 bp mRNA linear EST 29-JAN-1998  
LOCUS vt16h01.r1 Barstead mouse myotubes MRLB5 Mus musculus cDNA clone  
DEFINITION IMAGE:1163281 5' similar to SW:ATP6\_MOUSE P00848 ATP SYNTHASE A  
CHAIN : mRNA sequence.  
AA771119  
AA771119.1 GI:2822930  
EST.  
Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 67)  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Stepoe, M., Tan, F., Underwood, K., Moore, B.,  
Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LML ; contact the  
IMGB Consortium (info@image.llnl.gov) for further information.  
MGI:629193  
Trace considered overall poor quality  
Possible reversed clone; similarity on wrong strand  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .67  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C3H"  
/db\_xref="taxon:10090"  
/clone="IMAG:1163281"  
/cell\_line="C2C12"  
/lab\_host="DH10B"

/clone\_lib="Barstead mouse myotubes MRLB5"  
/note="vector: pRT3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: EcoRI; Site\_2: NotI; 1st strand cDNA  
was primed with a Not I - oligo(dt) primer (5'  
TGTTCGACATCTGAGAGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT  
3') ; double-stranded cDNA was ligated to Eco RI adaptors  
(AATTGGATCCTTG), digested with Not I and cloned into the  
Not I and Eco RI sites of the modified pRT3 vector.  
Library constructed by Bob Barstead. The C2C12 cell line  
(available from ATCC, catalog # CRL-1772) differentiates  
rapidly, forming contractile myotubes and producing  
characteristic muscle proteins."

BASE COUNT  
ORIGIN  
21 a 18 c 9 g 19 t

Query Match  
Best Local Similarity 85.7%; Score 10.8; DB 9; Length 67;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY  
3 GCTAGCTACACGA 16  
:|||||  
67 GATGCTACACGA 54

Db  
67 GATGCTACACGA 54

RESULT 38  
CB366166  
LOCUS  
DEFINITION ZF001-P00049-DPE-F2-D.F10 GISZF001 Danio rerio cDNA clone  
IMAGE:6910149 5' similar to fp15803.Y1 zebrafish gridded kidney  
Danio rerio cDNA clone IMAGE:472612 5' similar to WP:CE25522  
Y61A91A.E. mRNA sequence.  
CB366166  
CB366166.1 GI:29016477  
EST.  
Danio rerio (zebrafish)  
ORIGIN Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes  
; Cyprinidae; Danio.  
1 (bases 1 to 67)  
AUTHORS Mathavan, S., Wei, C., Thoreau, H., Chia, J.M. and Ruan, Y.  
TITLE Genome Institute of Singapore  
JOURNAL Genome Institute of Singapore, Zebrafish EST Collection  
COMMENT Unpublished  
Contact: Ruan Y  
Laboratory of Molecular Biotechnology  
Genome Institute of Singapore  
1 Science Park Road, The Capricorn #05-01, Singapore 117528  
Tel: +65 6827 5200  
Fax: +65 6827 5201  
Email: gisry@nus.edu.sg  
GIS Clone ID: ZF001-P00049-PP\_L20  
PCR Primers  
FORWARD: M13  
BACKWARD: M13  
Plate: ZF001-P00049-DPE-F2-D  
Seq primer: CGGATACCTTGATACGA  
High quality sequence stop: 67.  
Location/Qualifiers  
1. .67  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAG:6910149"  
/tissue\_type="Embryo"  
/dev\_stage="7 Different embryonic Stages ( From just  
fertilized Embryos to 72 hours just hatched baby fish )"  
/lab\_host="DH10B"  
/clone\_lib="GISZF001"  
/note="vector: pDNR-LIB, Site\_1: Sfi A (GGCCATTCAGCC);  
Site\_2: Sfi B (GGCGGCTCGCC); Priming method: Sfi-(dt)30  
primed ; Priming sequence: 5'ATTCAGA GGCGGAGGGCGCC  
GACATG(T)30VN ; Directionally cloned, 5' cloning site:  
Sfi A site GGCCATTCAGCC ; 5' linker/adaptor sequence:

5. AACGACTGCTATCAGCCAGAGTGGCC ; 3' cloning site: Sfi B site GGGCGGCTCGCC ; 3' linker/adaptor sequence: same as the priming sequence ; Average insert size: 2kb ; For PCR insert analysis: Use M13 Forward and reverse primers ; Library Amplified Recombinants (inserts) : 98% ; Library complexity: 5x10<sup>6</sup> ; Full-length construction (method) : SMART, a Clontech method ; Library constructed by: S. Mathavan, Chla-Lin Wei, and Yijun Ruan Genome Institute of Singapore"

BASE COUNT 19 a 19 c 14 g 15 t

ORIGIN

Query Match 67.5% ; Score 10.8 ; DB 14 ; Length 67 ; Best Local Similarity 75.0% ; Pred. No. 9e+04 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

Matches 12 ; Conservative 1 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

QY 1 RGGCTAGCTACAACA 16  
: |||||  
33 GGGCTAGCCACAACA 48

RESULT 39  
D11778/c 69 bp mRNA linear EST 02-DEC-1992  
LOCUS HUMH01E11 Liver HepG2 cell line. Homo sapiens CDNA clone hm01e11,  
DEFINITION mRNA sequence.  
ACCESSION D11778  
VERSION D11778.1 GI:2155059  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 69) Okubo, K., Hori, N., Matoba, R., Miyama, T., Fukushima, A., Kojima, Y. and Matsubara, K.  
TITLE Large scale CDNA sequencing for analysis of quantitative and qualitative aspects of gene expression  
JOURNAL Nat. Genet. 2, 173-179 (1992)  
MEDLINE 94258199  
PUBMED  
COMMENT Contact: Kouzaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Miyama, Atsushi Fukushima, Yoko Kojima & Kenichi Matsubara  
Institute for Molecular and Cellular Biology  
Osaka University  
1-3 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES  
source  
1..69  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:D088324E"  
/db\_xref="taxon:9606"  
/clone="hm01e11"  
/lab\_host="E.coli"  
/clone\_lib="Liver HepG2 cell line."  
/note="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli."

BASE COUNT 24 a 14 c 8 g 23 t

ORIGIN

Query Match 67.5% ; Score 10.8 ; DB 14 ; Length 69 ; Best Local Similarity 75.0% ; Pred. No. 9.1e+04 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

Matches 12 ; Conservative 1 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

QY 1 RGGCTAGCTACAACA 16  
: |||||  
20 AGGATGGCTACAACA 5

RESULT 40  
AM104004 71 bp mRNA linear EST 20-OCT-1999  
LOCUS AM104004  
DEFINITION x63h05.x1 NCI\_CGAP\_Ov23 Homo sapiens CDNA clone IMAGE:2598489 3',

mRNA sequence.  
AM104004  
AM104004.1 GI:6074739  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 71)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@email.nih.gov  
Tissue Procurement: Christopher Morkaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
1..71  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2598489"  
/issue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ov23"  
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"

BASE COUNT 24 a 8 c 14 g 25 t

ORIGIN

Query Match 67.5% ; Score 10.8 ; DB 9 ; Length 71 ; Best Local Similarity 75.0% ; Pred. No. 9.2e+04 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

Matches 12 ; Conservative 1 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

QY 1 RGGCTAGCTACAACA 16  
: |||||  
47 AGGATGGCTACAACA 62

Search completed: January 21, 2004, 08:16:07  
Job time : 148 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:45:02 ; Search time 38 Seconds

(without alignments)  
185.846 Million cell updates/sec

Title: US-09-423-035B-122

Perfect score: 16

Sequence: 1 rgsctacgacaaga 16

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 830498

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*\n2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*\n3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*\n4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*\n5: /cgn2\_6/ptodata/2/ina/PCITUS.COMB.seq:\*\n6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	92.5	16	4	US-09-536-393-19
2	14.8	92.5	16	4	US-09-536-393-20
3	14.8	92.5	29	4	US-09-270-140A-23
4	14.8	92.5	29	4	US-09-270-140A-25
5	14.8	92.5	30	4	US-09-270-140A-55
6	14.8	92.5	31	3	US-09-253-955-5
7	14.8	92.5	31	3	US-09-637-405-5
8	14.8	92.5	31	4	US-09-270-140A-42
9	14.8	92.5	31	4	US-09-270-140A-45
10	14.8	92.5	31	4	US-09-270-140A-48
11	14.8	92.5	31	4	US-09-270-140A-51
12	14.8	92.5	31	4	US-09-746-985B-5
13	14.8	92.5	32	4	US-09-270-140A-12
14	14.8	92.5	32	4	US-09-270-140A-15
15	14.8	92.5	32	4	US-09-270-140A-19
16	14.8	92.5	32	4	US-09-270-140A-28
17	14.8	92.5	32	4	US-09-270-140A-58
18	14.8	92.5	34	4	US-09-270-140A-9
19	14.8	92.5	34	4	US-09-270-140A-53
20	14.8	92.5	35	4	US-09-270-140A-3
21	14.8	92.5	35	4	US-09-270-140A-6
22	14.8	92.5	35	4	US-09-270-140A-31
23	14.8	92.5	35	4	US-09-270-140A-39
24	14.8	92.5	38	4	US-09-270-140A-34
25	14.8	92.5	39	4	US-09-270-140A-36
26	14.8	92.5	39	4	US-09-270-140A-91
27	14.8	92.5	39	4	US-09-270-140A-94

28	14.8	92.5	47	4	US-08-849-567A-85	Sequence 85, Appl
29	14.8	92.5	48	4	US-08-849-567A-87	Sequence 87, Appl
30	14.8	92.5	49	4	US-08-849-567A-81	Sequence 81, Appl
31	14.8	92.5	50	3	US-09-253-955-8	Sequence 8, Appl
32	14.8	92.5	50	3	US-09-637-405-8	Sequence 8, Appl
33	14.8	92.5	50	3	US-09-746-985B-8	Sequence 8, Appl
34	14.8	92.5	51	4	US-08-849-567A-86	Sequence 86, Appl
35	14.8	92.5	59	3	US-09-253-955-2	Sequence 2, Appl
36	14.8	92.5	59	3	US-09-637-405-2	Sequence 2, Appl
37	14.8	92.5	59	3	US-09-746-985B-2	Sequence 2, Appl
38	14.8	92.5	60	3	US-09-253-955-10	Sequence 10, Appl
39	14.8	92.5	60	3	US-09-637-405-10	Sequence 10, Appl
40	14.8	92.5	60	3	US-09-270-140A-95	Sequence 95, Appl
41	14.8	92.5	60	4	US-09-746-985B-10	Sequence 10, Appl
42	14.8	92.5	98	3	US-09-253-955-11	Sequence 11, Appl
43	14.8	92.5	98	3	US-09-637-405-11	Sequence 11, Appl
44	14.8	92.5	98	4	US-09-270-140A-96	Sequence 96, Appl
45	14.8	92.5	98	4	US-09-746-985B-11	Sequence 11, Appl
46	12.2	76.2	31	1	US-08-303-270-4	Sequence 4, Appl
47	11.6	72.5	30	3	US-09-242-797-5	Sequence 5, Appl
48	11.6	72.5	30	3	US-09-242-797-7	Sequence 7, Appl
49	11.6	72.5	48	3	US-09-997-918-43	Sequence 43, Appl
50	11.6	72.5	48	3	US-09-997-918-41	Sequence 41, Appl
51	11.6	72.5	50	3	US-09-292-071-3	Sequence 3, Appl
52	11.6	72.5	50	3	US-09-292-071-4	Sequence 4, Appl
53	11.6	72.5	50	3	US-09-292-069A-3	Sequence 3, Appl
54	11.6	72.5	50	3	US-09-292-069A-4	Sequence 4, Appl
55	11.6	72.5	50	3	US-09-418-721-3	Sequence 3, Appl
56	11.6	72.5	50	3	US-09-418-721-4	Sequence 4, Appl
57	11.6	72.5	50	4	US-09-767-013-3	Sequence 3, Appl
58	11.6	72.5	50	4	US-09-767-013-4	Sequence 4, Appl
59	11.6	72.5	50	4	US-09-292-072-3	Sequence 3, Appl
60	11.6	72.5	50	4	US-09-292-072-4	Sequence 4, Appl
61	11.6	72.5	50	4	US-09-170-496D-237	Sequence 23, App
62	11.6	72.5	55	4	US-09-170-496D-238	Sequence 23, App
63	11.6	72.5	55	3	US-08-997-918-48	Sequence 48, Appl
64	11.6	72.5	60	3	US-08-290-736C-37	Sequence 37, Appl
65	11.6	72.5	71	3	US-08-290-736C-46	Sequence 46, Appl
66	11.6	72.5	71	3	US-08-290-736C-47	Sequence 47, Appl
67	11.2	70.0	20	4	US-09-198-452A-4924	Sequence 4924, Ap
68	11.2	70.0	20	4	US-09-198-452A-6403	Sequence 6403, Ap
69	11.2	70.0	40	1	US-08-741-881-83	Sequence 83, Appl
70	11.2	70.0	40	1	US-08-739-158-83	Sequence 83, Appl
71	11.2	70.0	40	2	US-08-739-167-83	Sequence 83, Appl
72	11.2	70.0	40	2	US-08-404-786-83	Sequence 83, Appl
73	11.2	70.0	40	3	US-08-931-869-83	Sequence 83, Appl
74	11.2	70.0	40	3	US-09-350-399-83	Sequence 83, Appl
75	11.2	70.0	48	2	US-09-236-140A-83	Sequence 83, Appl
76	11.2	70.0	48	2	US-08-811-492-124	Sequence 124, App
77	11.2	70.0	55	1	US-08-180-195-10	Sequence 10, Appl
78	11.2	70.0	55	1	US-08-180-195-11	Sequence 11, Appl
79	11.2	70.0	55	1	US-08-477-329-10	Sequence 10, Appl
80	11.2	70.0	55	1	US-08-477-329-11	Sequence 11, Appl
81	11.2	70.0	55	2	US-08-811-492-125	Sequence 125, App
82	11.2	70.0	55	2	US-08-475-458-10	Sequence 10, Appl
83	11.2	70.0	55	2	US-08-475-458-11	Sequence 11, Appl
84	11.2	70.0	55	3	US-08-980-400-10	Sequence 10, Appl
85	11.2	70.0	55	3	US-08-980-400-11	Sequence 11, Appl
86	11.2	70.0	55	3	US-09-583-459A-10	Sequence 10, Appl
87	11.2	70.0	55	3	US-09-583-459A-11	Sequence 11, Appl
88	11.2	70.0	55	3	US-09-583-210-10	Sequence 10, Appl
89	11.2	70.0	55	3	US-09-583-210-11	Sequence 11, Appl
90	11.2	70.0	55	4	US-09-583-449A-10	Sequence 10, Appl
91	11.2	70.0	55	4	US-09-583-449A-11	Sequence 11, Appl
92	11.2	70.0	55	4	US-09-435-059-10	Sequence 10, Appl
93	11.2	70.0	55	4	US-09-435-059-11	Sequence 11, Appl
94	11.2	70.0	75	4	US-09-702-705-242	Sequence 242, App
95	11.2	68.8	75	4	US-09-736-457-242	Sequence 247, App
96	11.2	68.8	78	4	US-09-702-705-1277	Sequence 1277, Ap
97	11.2	68.8	78	4	US-09-736-457-1277	Sequence 1277, Ap
98	10.8	67.5	27	3	US-08-981-189B-18	Sequence 18, Appl
99	10.8	67.5	33	4	US-09-523-686-6	Sequence 6, Appl
100	10.8	67.5	42	3	US-09-079-984A-5	Sequence 5, Appl



247	10	62.5	47	4	US-09-361-727-4	Sequence 4, Appl1	320	9.6	60.0	21	4	US-09-091-952a-80	Sequence 80, Appl1
C 248	10	62.5	47	4	US-09-641-638-1061	Sequence 1061, Ap	321	9.6	60.0	21	4	US-09-422-978-10259	Sequence 10259, A
249	10	62.5	47	4	US-09-422-978-858	Sequence 858, App	C 322	9.6	60.0	23	1	US-08-244-269-3	Sequence 3, Appl1
250	10	62.5	50	1	US-08-519-197-5	Sequence 5, Appl1	C 323-	9.6	60.0	23	1	US-08-348-683-16	Sequence 16, Appl1
251	10	62.5	50	4	US-09-554-929-69	Sequence 69, Appl1	C 324	9.6	60.0	23	4	US-09-207-388-66	Sequence 66, Appl1
C 252	10	62.5	50	5	PCT-US95-11405-17	Sequence 17, Appl1	C 325	9.6	60.0	24	2	US-08-659-998-90	Sequence 90, Appl1
253	10	62.5	51	1	US-08-688-609-13	Sequence 13, Appl1	C 326	9.6	60.0	24	4	US-09-225-928-90	Sequence 90, Appl1
254	10	62.5	51	3	US-09-002-832-13	Sequence 13, Appl1	C 327	9.6	60.0	24	4	US-09-225-201B-90	Sequence 90, Appl1
C 255	10	62.5	53	2	US-08-657-382-32	Sequence 32, Appl1	328	9.6	60.0	25	1	US-08-244-269-4	Sequence 4, Appl1
C 256	10	62.5	53	4	PCT-US94-02539-32	Sequence 32, Appl1	329	9.6	60.0	25	1	US-08-244-269-6	Sequence 6, Appl1
C 257	10	62.5	54	5	US-09-479-645A-218	Sequence 218, App	330	9.6	60.0	25	1	US-08-348-683-18	Sequence 18, Appl1
258	10	62.5	62	1	US-08-366-783-13	Sequence 66, Appl1	331	9.6	60.0	25	1	US-08-093-741-38	Sequence 19, Appl1
259	10	62.5	62	1	US-08-846-021A-17	Sequence 17, Appl1	332	9.6	60.0	26	1	US-08-720-012-38	Sequence 38, Appl1
260	10	62.5	62	2	US-07-807-529A-16	Sequence 16, Appl1	333	9.6	60.0	26	2	US-08-560-098A-31	Sequence 31, Appl1
261	10	62.5	63	3	US-08-300-928C-65	Sequence 65, Appl1	334	9.6	60.0	26	3	US-08-967-024C-19	Sequence 19, Appl1
262	10	62.5	63	3	US-08-430-944D-65	Sequence 65, Appl1	335	9.6	60.0	26	3	US-09-306-005-13	Sequence 13, Appl1
263	10	62.5	63	3	US-08-430-014-65	Sequence 65, Appl1	336	9.6	60.0	26	3	US-09-253-316-34	Sequence 34, Appl1
264	10	62.5	63	3	US-08-431-184-65	Sequence 65, Appl1	337	9.6	60.0	27	4	US-09-457-066-33	Sequence 33, Appl1
265	10	62.5	63	3	US-08-465-591A-67	Sequence 67, Appl1	338	9.6	60.0	27	4	US-09-564-595D-31	Sequence 31, Appl1
C 266	10	62.5	71	2	US-08-465-594A-67	Sequence 67, Appl1	339	9.6	60.0	27	4	US-09-706-968-33	Sequence 33, Appl1
C 267	10	62.5	71	2	US-08-973-124-252	Sequence 252, App	340	9.6	60.0	27	4	US-09-585-228-17	Sequence 17, Appl1
C 268	10	62.5	71	3	PCT-US96-08014-252	Sequence 252, App	341	9.6	60.0	27	4	US-08-816-693A-42	Sequence 42, Appl1
C 269	10	62.5	74	3	US-09-315-794-2	Sequence 2, Appl1	342	9.6	60.0	29	2	US-08-885-291-42	Sequence 42, Appl1
C 270	10	62.5	74	3	US-09-389-341-2	Sequence 2, Appl1	343	9.6	60.0	29	3	US-09-496-672-42	Sequence 42, Appl1
C 271	10	62.5	79	1	US-08-472-255A-139	Sequence 139, App	344	9.6	60.0	30	1	US-08-049-473-15	Sequence 15, Appl1
272	10	62.5	79	1	US-08-472-255A-165	Sequence 165, App	345	9.6	60.0	30	1	US-08-049-473-15	Sequence 15, Appl1
273	10	62.5	79	1	US-08-479-724A-139	Sequence 139, App	C 346	9.6	60.0	30	1	US-08-049-473-15	Sequence 15, Appl1
274	10	62.5	79	1	US-08-479-724A-139	Sequence 139, App	347	9.6	60.0	30	1	US-08-312-648-11	Sequence 11, Appl1
275	10	62.5	79	1	US-08-479-724A-165	Sequence 165, App	C 348	9.6	60.0	30	1	US-08-312-648-11	Sequence 11, Appl1
276	10	62.5	79	3	US-08-472-256B-139	Sequence 139, App	C 349	9.6	60.0	30	3	US-08-913-842-51	Sequence 51, Appl1
277	10	62.5	79	3	US-08-472-256B-165	Sequence 165, App	350	9.6	60.0	30	3	US-09-176-862-7	Sequence 7, Appl1
278	10	62.5	79	3	US-08-952-793-139	Sequence 139, App	351	9.6	60.0	30	3	US-09-202-316-43	Sequence 43, Appl1
279	10	62.5	79	3	US-08-952-793-165	Sequence 165, App	352	9.6	60.0	30	5	PCT-US94-04190-16	Sequence 16, Appl1
280	10	62.5	79	4	US-09-849-928-165	Sequence 139, App	C 353	9.6	60.0	30	5	PCT-US94-04190-16	Sequence 16, Appl1
281	10	62.5	79	4	US-09-849-928-165	Sequence 139, App	C 354	9.6	60.0	31	4	US-08-628-665-13	Sequence 13, Appl1
282	10	62.5	79	5	PCT-US96-09455A-139	Sequence 139, App	355	9.6	60.0	32	1	US-08-628-665-13	Sequence 13, Appl1
283	10	62.5	79	5	PCT-US96-09455A-165	Sequence 165, App	C 356	9.6	60.0	33	1	US-08-309-560-24	Sequence 24, Appl1
284	10	62.5	83	3	US-09-133-944-3	Sequence 3, Appl1	C 357	9.6	60.0	33	1	US-07-977-696C-57	Sequence 57, Appl1
285	10	62.5	83	4	US-09-208-827-3	Sequence 3, Appl1	C 358	9.6	60.0	33	1	US-08-129-530B-57	Sequence 57, Appl1
C 286	10	62.5	84	1	US-07-745-206A-10	Sequence 10, Appl1	C 359	9.6	60.0	33	2	US-08-583-562B-22	Sequence 22, Appl1
C 287	10	62.5	84	1	US-08-455-543A-6	Sequence 6, Appl1	C 360	9.6	60.0	33	2	US-08-779-113-32	Sequence 32, Appl1
C 288	10	62.5	84	2	US-08-193-078B-6	Sequence 6, Appl1	C 361	9.6	60.0	33	2	US-08-930-605-8	Sequence 8, Appl1
C 289	10	62.5	84	2	US-08-223-305C-6	Sequence 6, Appl1	C 362	9.6	60.0	33	4	US-08-976-288A-57	Sequence 57, Appl1
C 290	10	62.5	84	2	US-08-149-097D-6	Sequence 6, Appl1	363	9.6	60.0	33	4	US-09-813-781-22	Sequence 22, Appl1
C 291	10	62.5	84	2	US-08-311-363-10	Sequence 10, Appl1	C 364	9.6	60.0	33	5	PCT-US94-05821A-24	Sequence 24, Appl1
C 292	10	62.5	84	3	US-08-949-386-6	Sequence 6, Appl1	C 365	9.6	60.0	34	1	US-08-434-503-13	Sequence 13, Appl1
C 293	10	62.5	84	3	US-08-450-562-6	Sequence 6, Appl1	C 366	9.6	60.0	34	1	US-08-628-665-15	Sequence 15, Appl1
C 294	10	62.5	84	4	US-08-984-709A-6	Sequence 6, Appl1	367	9.6	60.0	36	1	US-08-197-791-23	Sequence 23, Appl1
C 295	10	62.5	84	4	US-08-450-272-6	Sequence 6, Appl1	368	9.6	60.0	36	1	US-08-399-696-15	Sequence 15, Appl1
C 296	10	62.5	88	4	US-09-351-814-6	Sequence 6, Appl1	369	9.6	60.0	36	4	US-09-371-772B-12826	Sequence 12826, A
C 297	9.8	61.3	19	1	US-08-379-081B-140	Sequence 140, App	370	9.6	60.0	39	2	US-08-723-306-12	Sequence 12, Appl1
C 298	9.8	61.3	19	1	US-08-379-078-140	Sequence 140, App	371	9.6	60.0	39	5	PCT-US96-10041-12	Sequence 12, Appl1
C 299	9.8	61.3	76	3	US-09-390-867A-6	Sequence 6, Appl1	372	9.6	60.0	40	2	US-08-882-083-4	Sequence 4, Appl1
C 300	9.8	61.3	76	4	US-09-548-260-6	Sequence 6, Appl1	373	9.6	60.0	40	2	US-08-558-107-4	Sequence 4, Appl1
C 301	9.8	61.3	87	3	US-09-390-867A-1	Sequence 1, Appl1	374	9.6	60.0	40	3	US-09-243-539-9	Sequence 9, Appl1
C 302	9.8	61.3	87	3	US-09-348-260-1	Sequence 1, Appl1	C 375	9.6	60.0	40	4	US-09-330-235-9	Sequence 4, Appl1
C 303	9.8	61.3	100	4	US-08-706-945D-91	Sequence 91, Appl1	C 376	9.6	60.0	42	3	US-08-897-527-1	Sequence 1, Appl1
C 304	9.6	60.0	18	1	US-08-093-741-37	Sequence 37, Appl1	377	9.6	60.0	42	3	US-09-072-508-1	Sequence 1, Appl1
C 305	9.6	60.0	18	1	US-08-720-012-37	Sequence 37, Appl1	C 378	9.6	60.0	44	1	US-08-399-696-65	Sequence 65, Appl1
C 306	9.6	60.0	18	2	US-08-560-098A-30	Sequence 30, Appl1	C 379	9.6	60.0	45	3	US-09-363-970-26	Sequence 26, Appl1
C 307	9.6	60.0	18	3	US-08-967-024C-18	Sequence 18, Appl1	C 380	9.6	60.0	46	1	US-07-994-659A-56	Sequence 56, Appl1
C 308	9.6	60.0	19	2	US-08-556-607-4	Sequence 4, Appl1	C 381	9.6	60.0	47	4	US-09-422-978-933	Sequence 933, App
C 309	9.6	60.0	20	1	US-07-922-723A-42	Sequence 42, Appl1	382	9.6	60.0	47	4	US-09-422-978-959	Sequence 959, App
C 310	9.6	60.0	20	1	US-07-799-828C-42	Sequence 42, Appl1	383	9.6	60.0	47	4	US-09-422-978-1217	Sequence 1217, App
C 311	9.6	60.0	20	2	US-07-953-277A-42	Sequence 42, Appl1	384	9.6	60.0	47	4	US-09-422-978-3244	Sequence 3244, Ap
312	9.6	60.0	20	3	US-09-289-267-68	Sequence 68, Appl1	C 385	9.6	60.0	48	1	US-07-609-716-37	Sequence 37, Appl1
313	9.6	60.0	20	3	US-09-101-886B-88	Sequence 88, Appl1	C 386	9.6	60.0	48	2	US-07-609-716-38	Sequence 38, Appl1
314	9.6	60.0	21	2	US-08-946-241B-5	Sequence 5, Appl1	C 387	9.6	60.0	48	2	US-08-882-083-3	Sequence 3, Appl1
315	9.6	60.0	21	3	US-09-309-053-5	Sequence 5, Appl1	C 388	9.6	60.0	48	2	US-08-558-107-3	Sequence 3, Appl1
316	9.6	60.0	21	3	US-08-109-037-15	Sequence 15, Appl1	C 389	9.6	60.0	48	3	US-09-243-539-3	Sequence 3, Appl1
317	9.6	60.0	21	3	US-08-109-037-88	Sequence 88, Appl1	C 390	9.6	60.0	48	3	US-08-475-111A-37	Sequence 37, Appl1
C 318	9.6	60.0	21	3	US-08-109-037-89	Sequence 89, Appl1	391	9.6	60.0	48	3	US-08-475-111A-38	Sequence 38, Appl1
C 319	9.6	60.0	21	3	US-08-109-037-90	Sequence 90, Appl1	C 392	9.6	60.0	48	3	US-08-478-029A-37	Sequence 37, Appl1

393	9.6	60.0	48	3	US-08-478-029A-38	Sequence 38, Appl	466	9.4	58.8	30	4	US-09-004-422-45	Sequence 45, Appl
394	9.6	60.0	49	1	US-08-644-271-26	Sequence 26, Appl	467	9.4	58.8	30	4	US-09-004-422-53	Sequence 53, Appl
395	9.6	60.0	49	3	US-09-363-970-27	Sequence 27, Appl	468	9.4	58.8	33	1	US-07-979-966A-16	Sequence 16, Appl
396	9.6	60.0	49	4	US-09-077-955-23	Sequence 23, Appl	469	9.4	58.8	36	1	US-08-147-000B-14	Sequence 14, Appl
397	9.6	60.0	50	1	US-07-994-469A-25	Sequence 25, Appl	470	9.4	58.8	37	1	US-07-621-193A-12	Sequence 12, Appl
398	9.6	60.0	50	1	US-08-445-640-20	Sequence 20, Appl	471	9.4	58.8	37	1	US-08-018-489C-12	Sequence 12, Appl
399	9.6	60.0	50	1	US-08-170-558-50	Sequence 50, Appl	472	9.4	58.8	44	3	US-09-227-850-11	Sequence 11, Appl
400	9.6	60.0	50	3	US-08-447-314-20	Sequence 20, Appl	473	9.4	58.8	45	1	US-08-450-332-3	Sequence 3, Appl
401	9.6	60.0	50	3	US-08-445-461-20	Sequence 20, Appl	474	9.4	58.8	45	2	US-08-637-640-3	Sequence 3, Appl
402	9.6	60.0	52	1	US-07-994-469A-35	Sequence 35, Appl	475	9.4	58.8	46	2	US-09-004-406C-3	Sequence 5, Appl
403	9.6	60.0	58	3	US-08-833-167-22	Sequence 22, Appl	476	9.4	58.8	47	1	US-07-749-446-5	Sequence 5, Appl
404	9.6	60.0	63	4	US-09-344-837A-22	Sequence 22, Appl	477	9.4	58.8	47	1	US-09-432-978-77A	Sequence 277A, Ap
405	9.6	60.0	63	4	US-08-833-167-20	Sequence 20, Appl	478	9.4	58.8	48	1	US-07-959-284-17	Sequence 17, Appl
406	9.6	60.0	64	4	US-09-344-837A-20	Sequence 20, Appl	479	9.4	58.8	48	2	US-08-308-736A-17	Sequence 17, Appl
407	9.6	60.0	64	4	US-09-180-827-15	Sequence 15, Appl	480	9.4	58.8	48	4	US-08-645-107A-17	Sequence 17, Appl
408	9.6	60.0	69	4	US-09-011-336-65	Sequence 65, Appl	481	9.4	58.8	48	4	US-09-197-349-17	Sequence 17, Appl
409	9.6	60.0	73	1	US-08-208-886C-18	Sequence 18, Appl	482	9.4	58.8	48	4	US-09-031-693-17	Sequence 17, Appl
410	9.6	60.0	73	1	US-08-704-744-18	Sequence 18, Appl	483	9.4	58.8	48	5	PCT-US93-09649A-17	Sequence 17, Appl
411	9.6	60.0	73	1	US-08-469-557-18	Sequence 18, Appl	484	9.4	58.8	48	5	PCT-US93-09649A-17	Sequence 17, Appl
412	9.6	60.0	73	2	US-08-290-793B-18	Sequence 18, Appl	485	9.4	58.8	48	5	PCT-US93-09649A-17	Sequence 17, Appl
413	9.6	60.0	75	1	US-08-219-012-87	Sequence 87, Appl	486	9.4	58.8	51	1	US-08-530-492-125	Sequence 125, App
414	9.6	60.0	75	3	US-08-687-421-275	Sequence 275, App	487	9.4	58.8	51	3	US-08-506-517-125	Sequence 6, Appl
415	9.6	60.0	75	3	US-09-060-756-163	Sequence 163, App	488	9.4	58.8	61	1	US-08-465-687A-6	Sequence 6, Appl
416	9.6	60.0	75	3	US-09-060-756-163	Sequence 163, App	489	9.4	58.8	61	3	US-08-465-687A-6	Sequence 6, Appl
417	9.6	60.0	79	4	US-09-023-228B-14	Sequence 14, Appl	490	9.4	58.8	63	4	US-09-520-210-6	Sequence 6, Appl
418	9.6	60.0	79	4	US-09-163-025B-14	Sequence 14, Appl	491	9.4	58.8	63	4	US-09-520-210-6	Sequence 6, Appl
419	9.6	60.0	79	4	US-10-037-882-14	Sequence 14, Appl	492	9.4	58.8	71	1	US-08-400-440A-101	Sequence 101, Appl
420	9.6	60.0	84	4	US-09-313-894A-3374	Sequence 3974, Ap	493	9.4	58.8	71	1	US-08-400-440A-101	Sequence 101, Appl
421	9.6	60.0	85	1	US-07-741-931-5	Sequence 5, Appl	494	9.4	58.8	71	1	US-08-463-093A-96	Sequence 96, Appl
422	9.6	60.0	85	1	US-07-937-132A-5	Sequence 5, Appl	495	9.4	58.8	71	1	US-08-463-093A-96	Sequence 96, Appl
423	9.6	60.0	86	1	US-07-937-132A-6	Sequence 6, Appl	496	9.4	58.8	71	2	US-08-460-888A-96	Sequence 96, Appl
424	9.6	60.0	86	1	US-07-741-931-7	Sequence 7, Appl	497	9.4	58.8	71	2	US-08-460-888A-96	Sequence 96, Appl
425	9.6	60.0	87	1	US-07-937-132A-7	Sequence 7, Appl	498	9.4	58.8	71	2	US-08-460-888A-96	Sequence 96, Appl
426	9.6	60.0	87	1	US-08-433-126A-108	Sequence 108, App	499	9.4	58.8	71	2	US-08-460-888A-96	Sequence 96, Appl
427	9.6	60.0	87	1	US-08-433-126A-108	Sequence 108, App	500	9.4	58.8	71	2	US-08-460-888A-96	Sequence 96, Appl
428	9.6	60.0	87	5	US-08-976-413A-108	Sequence 108, App	501	9.4	58.8	71	4	US-09-412-017-96	Sequence 101, Appl
429	9.6	60.0	87	5	PCT-US96-06059-108	Sequence 108, App	502	9.4	58.8	71	4	US-09-412-017-96	Sequence 101, Appl
430	9.6	60.0	90	1	US-08-317-748A-18	Sequence 18, Appl	503	9.4	58.8	79	3	US-08-887-421-399	Sequence 399, App
431	9.6	60.0	90	1	US-08-471-985A-18	Sequence 18, Appl	504	9.4	58.8	86	1	US-07-964-624D-59	Sequence 59, Appl
432	9.6	60.0	90	5	PCT-US95-12401A-18	Sequence 11, Appl	505	9.4	58.8	86	1	US-08-442-062-59	Sequence 59, Appl
433	9.6	60.0	92	3	US-09-129-740-7	Sequence 7, Appl	506	9.4	58.8	86	1	US-08-748-697A-59	Sequence 59, Appl
434	9.6	60.0	92	3	US-09-568-527-7	Sequence 7, Appl	507	9.4	58.8	90	3	US-09-165-616-59	Sequence 59, Appl
435	9.6	60.0	98	5	PCT-US94-06456-11	Sequence 34, Appl	508	9.4	58.8	93	3	US-08-483-511-33	Sequence 33, Appl
436	9.6	60.0	98	5	PCT-US94-06456-11	Sequence 34, Appl	509	9.4	58.8	93	3	PCT-US93-01009-33	Sequence 33, Appl
437	9.6	60.0	100	3	US-08-145-705A-34	Sequence 37, Appl	510	9.4	58.8	100	1	US-08-976-413A-434	Sequence 434, App
438	9.6	60.0	18	3	US-09-197-380-37	Sequence 7, Appl	511	9.2	57.5	17	3	US-09-027-998A-41	Sequence 41, Appl
439	9.4	58.8	20	1	US-08-099-868-7	Sequence 7, Appl	512	9.2	57.5	19	3	US-09-058-488A-57	Sequence 57, Appl
440	9.4	58.8	20	2	US-07-977-284A-78	Sequence 78, Appl	513	9.2	57.5	20	1	US-07-829-016-9	Sequence 1, Appl
441	9.4	58.8	21	2	US-08-600-999-7	Sequence 9, Appl	514	9.2	57.5	20	1	US-08-062-633-1	Sequence 1, Appl
442	9.4	58.8	21	2	US-08-600-999-9	Sequence 11, Appl	515	9.2	57.5	20	1	US-08-487-651-9	Sequence 9, Appl
443	9.4	58.8	21	2	US-09-082-762-11	Sequence 11, Appl	516	9.2	57.5	20	2	US-08-487-645A-9	Sequence 9, Appl
444	9.4	58.8	21	4	US-08-448-256-21	Sequence 21, Appl	517	9.2	57.5	20	2	US-09-444-053-52	Sequence 52, Appl
445	9.4	58.8	22	1	US-08-599-252-36	Sequence 36, Appl	518	9.2	57.5	20	4	US-09-732-199A-51	Sequence 51, Appl
446	9.4	58.8	22	1	US-08-182-172-17	Sequence 17, Appl	519	9.2	57.5	20	4	US-09-198-452A-222	Sequence 222, Ap
447	9.4	58.8	22	5	PCT-US96-06352-36	Sequence 36, Appl	520	9.2	57.5	21	3	US-09-023-025-32	Sequence 32, Appl
448	9.4	58.8	22	5	PCT-US96-06352-36	Sequence 36, Appl	521	9.2	57.5	21	3	US-09-023-025-32	Sequence 32, Appl
449	9.4	58.8	22	5	PCT-US96-06352-36	Sequence 36, Appl	522	9.2	57.5	21	3	US-08-335-844A-61	Sequence 61, Appl
450	9.4	58.8	24	2	US-08-202-033-10	Sequence 10, Appl	523	9.2	57.5	21	4	US-08-937-378-21	Sequence 21, Appl
451	9.4	58.8	24	2	US-08-548-974-10	Sequence 10, Appl	524	9.2	57.5	21	4	US-08-977-378-21	Sequence 21, Appl
452	9.4	58.8	24	4	US-08-637-823B-10	Sequence 10, Appl	525	9.2	57.5	21	4	US-08-937-378-21	Sequence 21, Appl
453	9.4	58.8	24	4	US-09-614-957D-10	Sequence 10, Appl	526	9.2	57.5	22	1	US-09-129-366-61	Sequence 61, Appl
454	9.4	58.8	24	4	US-08-637-823B-10	Sequence 10, Appl	527	9.2	57.5	22	1	US-08-283-203-17	Sequence 17, Appl
455	9.4	58.8	27	3	US-08-403-555-1	Sequence 1, Appl	528	9.2	57.5	23	1	US-08-078-222B-6	Sequence 6, Appl
456	9.4	58.8	27	3	US-09-331-581-12	Sequence 12, Appl	529	9.2	57.5	23	2	US-08-661-330A-6	Sequence 6, Appl
457	9.4	58.8	29	3	US-08-506-553C-10	Sequence 10, Appl	530	9.2	57.5	23	3	US-09-038-217A-6	Sequence 6, Appl
458	9.4	58.8	29	3	US-09-382-155-37	Sequence 37, Appl	531	9.2	57.5	23	3	US-09-476-239-43	Sequence 43, Appl
459	9.4	58.8	29	3	US-08-382-155-38	Sequence 38, Appl	532	9.2	57.5	23	4	US-09-609-154-43	Sequence 43, Appl
460	9.4	58.8	30	1	US-08-361-920-17	Sequence 17, Appl	533	9.2	57.5	23	4	US-09-609-154-43	Sequence 43, Appl
461	9.4	58.8	30	1	US-08-229-781-45	Sequence 45, Appl	534	9.2	57.5	23	4	US-09-447-034-6	Sequence 6, Appl
462	9.4	58.8	30	1	US-08-630-918-53	Sequence 53, Appl	535	9.2	57.5	24	1	US-08-520-928-3	Sequence 3, Appl
463	9.4	58.8	30	1	US-08-630-918-53	Sequence 53, Appl	536	9.2	57.5	24	1	US-08-880-829-17	Sequence 17, Appl
464	9.4	58.8	30	1	US-08-479-939-77	Sequence 77, Appl	537	9.2	57.5	24	2	US-08-880-829-19	Sequence 19, Appl
465	9.4	58.8	30	1	US-08-483-432-77	Sequence 77, Appl	538	9.2	57.5	24	3	US-08-526-136-6	Sequence 6, Appl

539	9.2	57.5	24	US-09-006-755B-10	Sequence 10, Appl	C 612	9.2	57.5	50	US-08-961-309-34	Sequence 34, Appl
C 540	9.2	57.5	25	US-08-986-727-26	Sequence 26, Appl	C 613	9.2	57.5	51	US-08-889-502-30	Sequence 30, Appl
C 541	9.2	57.5	26	US-09-534-638-16	Sequence 16, Appl	C 614	9.2	57.5	51	US-08-403-416A-14	Sequence 14, Appl
C 542	9.2	57.5	26	US-09-733-199A-6	Sequence 6, Appl	C 615	9.2	57.5	52	US-08-889-502-29	Sequence 29, Appl
C 543	9.2	57.5	26	US-09-538-709-34	Sequence 34, Appl	C 616	9.2	57.5	52	US-09-027-998A-18	Sequence 18, Appl
C 544	9.2	57.5	27	US-08-678-304-7	Sequence 7, Appl	C 617	9.2	57.5	52	US-09-027-998A-19	Sequence 19, Appl
C 545	9.2	57.5	27	US-09-253-316-34	Sequence 34, Appl	C 618	9.2	57.5	54	US-08-832-535-8	Sequence 8, Appl
C 546	9.2	57.5	27	US-09-457-066-33	Sequence 33, Appl	C 619	9.2	57.5	54	US-09-019-485-15	Sequence 15, Appl
C 547	9.2	57.5	27	US-09-564-595D-31	Sequence 31, Appl	C 620	9.2	57.5	54	US-09-528-436B-14	Sequence 14, Appl
C 548	9.2	57.5	27	US-09-706-968-33	Sequence 33, Appl	C 621	9.2	57.5	55	US-08-362-525-9	Sequence 9, Appl
C 549	9.2	57.5	27	US-09-585-228-17	Sequence 17, Appl	C 622	9.2	57.5	55	US-08-362-525-10	Sequence 10, Appl
C 550	9.2	57.5	28	US-08-683-743-16	Sequence 16, Appl	C 623	9.2	57.5	59	US-08-891-292A-34	Sequence 34, Appl
C 551	9.2	57.5	28	US-08-600-999-10	Sequence 10, Appl	C 624	9.2	57.5	59	US-08-891-292A-32	Sequence 32, Appl
C 552	9.2	57.5	29	US-08-537-402-3	Sequence 3, Appl	C 625	9.2	57.5	59	US-09-927-737C-32	Sequence 32, Appl
C 553	9.2	57.5	29	US-08-233-016-13	Sequence 13, Appl	C 626	9.2	57.5	59	US-09-927-737C-34	Sequence 34, Appl
C 554	9.2	57.5	29	US-09-121-539-4	Sequence 4, Appl	C 627	9.2	57.5	60	US-08-687-916-26	Sequence 26, Appl
C 555	9.2	57.5	29	US-09-121-539-5	Sequence 5, Appl	C 628	9.2	57.5	60	US-09-138-614-26	Sequence 26, Appl
C 556	9.2	57.5	30	US-08-600-999-8	Sequence 8, Appl	C 629	9.2	57.5	62	US-08-956-182-25	Sequence 25, Appl
C 557	9.2	57.5	30	US-08-666-354A-8	Sequence 8, Appl	C 630	9.2	57.5	65	US-08-986-727-16	Sequence 16, Appl
C 558	9.2	57.5	30	US-09-374-038-9	Sequence 9, Appl	C 631	9.2	57.5	67	US-08-771-624B-18	Sequence 18, Appl
C 559	9.2	57.5	30	US-09-688-179-9	Sequence 9, Appl	C 632	9.2	57.5	69	US-08-184-009-101	Sequence 101, Appl
C 560	9.2	57.5	30	US-09-528-279-23	Sequence 23, Appl	C 633	9.2	57.5	69	US-08-458-356-101	Sequence 101, Appl
C 561	9.2	57.5	30	US-09-538-709-20	Sequence 20, Appl	C 634	9.2	57.5	69	US-08-460-736-101	Sequence 101, Appl
C 562	9.2	57.5	32	US-10-158-895-23	Sequence 23, Appl	C 635	9.2	57.5	69	US-09-535-370-101	Sequence 2, Appl
C 563	9.2	57.5	32	US-08-880-829-8	Sequence 8, Appl	C 636	9.2	57.5	70	US-08-277-547-2	Sequence 2, Appl
C 564	9.2	57.5	33	US-08-438-639-55	Sequence 55, Appl	C 637	9.2	57.5	70	US-08-880-829-13	Sequence 13, Appl
C 565	9.2	57.5	33	US-07-813-338A-55	Sequence 55, Appl	C 638	9.2	57.5	70	US-08-880-829-12	Sequence 12, Appl
C 566	9.2	57.5	34	US-08-956-182-37	Sequence 37, Appl	C 639	9.2	57.5	70	PCT-US95-08782-2	Sequence 2, Appl
C 567	9.2	57.5	36	US-08-585-585A-13	Sequence 13, Appl	C 640	9.2	57.5	71	US-08-584-760A-35	Sequence 35, Appl
C 568	9.2	57.5	36	US-08-687-916-27	Sequence 27, Appl	C 641	9.2	57.5	73	US-08-880-829-12	Sequence 12, Appl
C 569	9.2	57.5	36	US-08-685-808-12	Sequence 12, Appl	C 642	9.2	57.5	78	US-08-729-601A-20	Sequence 20, Appl
C 570	9.2	57.5	36	US-08-505-860C-12	Sequence 12, Appl	C 643	9.2	57.5	78	US-07-982-712-10	Sequence 10, Appl
C 571	9.2	57.5	36	US-09-138-614-27	Sequence 27, Appl	C 644	9.2	57.5	80	US-09-039-555B-4	Sequence 4, Appl
C 572	9.2	57.5	37	US-08-150-331-8	Sequence 8, Appl	C 645	9.2	57.5	83	US-08-977-778-20	Sequence 20, Appl
C 573	9.2	57.5	37	US-08-150-331-29	Sequence 29, Appl	C 646	9.2	57.5	86	US-08-976-413A-34	Sequence 34, Appl
C 574	9.2	57.5	37	US-08-569-284-8	Sequence 8, Appl	C 647	9.2	57.5	87	US-08-433-126A-226	Sequence 226, Appl
C 575	9.2	57.5	37	US-08-569-284-29	Sequence 29, Appl	C 648	9.2	57.5	87	US-08-433-126A-226	Sequence 226, Appl
C 576	9.2	57.5	39	US-08-464-531-105	Sequence 105, Appl	C 649	9.2	57.5	87	US-08-976-413A-226	Sequence 226, Appl
C 577	9.2	57.5	39	US-08-461-598-105	Sequence 105, Appl	C 650	9.2	57.5	87	PCT-US96-06059-226	Sequence 226, Appl
C 578	9.2	57.5	39	US-08-322-137-105	Sequence 105, Appl	C 651	9.2	57.5	89	US-07-964-624D-31	Sequence 31, Appl
C 579	9.2	57.5	39	US-08-582-333A-41	Sequence 41, Appl	C 652	9.2	57.5	89	US-08-442-062-31	Sequence 31, Appl
C 580	9.2	57.5	40	US-08-362-525-6	Sequence 6, Appl	C 653	9.2	57.5	89	US-08-748-697A-31	Sequence 31, Appl
C 581	9.2	57.5	42	US-08-466-860-41	Sequence 41, Appl	C 654	9.2	57.5	89	US-09-165-616-31	Sequence 31, Appl
C 582	9.2	57.5	42	US-08-472-040A-41	Sequence 41, Appl	C 655	9.2	57.5	95	US-08-789-333F-96	Sequence 96, Appl
C 583	9.2	57.5	42	US-08-276-776-41	Sequence 41, Appl	C 656	9.2	57.5	95	US-08-787-738B-96	Sequence 96, Appl
C 584	9.2	57.5	42	US-08-471-209-41	Sequence 41, Appl	C 657	9.2	57.5	99	US-09-035-220-2	Sequence 2, Appl
C 585	9.2	57.5	44	US-09-027-998A-12	Sequence 12, Appl	C 658	9.2	57.5	14	US-09-275-850-23	Sequence 23, Appl
C 586	9.2	57.5	44	US-09-027-998A-13	Sequence 13, Appl	C 659	9.2	56.2	15	US-08-311-486C-61	Sequence 61, Appl
C 587	9.2	57.5	45	US-09-027-998A-9	Sequence 9, Appl	C 660	9.2	56.2	15	US-09-275-850-17	Sequence 17, Appl
C 588	9.2	57.5	45	US-09-027-998A-10	Sequence 10, Appl	C 661	9.2	56.2	17	US-08-584-040-2622	Sequence 2622, Appl
C 589	9.2	57.5	45	US-09-027-998A-15	Sequence 15, Appl	C 662	9.2	56.2	17	US-08-584-040-2623	Sequence 2623, Appl
C 590	9.2	57.5	45	US-09-027-998A-16	Sequence 16, Appl	C 663	9.2	56.2	17	US-09-371-772B-1146	Sequence 1146, Appl
C 591	9.2	57.5	46	US-08-977-378-19	Sequence 19, Appl	C 664	9.2	56.2	17	US-09-371-772B-1147	Sequence 1147, Appl
C 592	9.2	57.5	47	US-09-671-317-574	Sequence 574, Appl	C 665	9.2	56.2	18	US-09-197-008-21	Sequence 21, Appl
C 593	9.2	57.5	47	US-09-422-978-583	Sequence 583, Appl	C 666	9.2	56.2	18	US-09-394-455-49	Sequence 49, Appl
C 594	9.2	57.5	47	US-09-422-978-2566	Sequence 2566, Appl	C 667	9.2	56.2	18	US-08-432-978-7271	Sequence 7271, Appl
C 595	9.2	57.5	48	US-08-171-389-200	Sequence 200, Appl	C 668	9.2	56.2	19	US-08-433-783-36	Sequence 36, Appl
C 596	9.2	57.5	48	US-08-123-936-200	Sequence 200, Appl	C 669	9.2	56.2	19	US-08-317-358-36	Sequence 36, Appl
C 597	9.2	57.5	48	US-08-475-228A-200	Sequence 200, Appl	C 670	9.2	56.2	19	PCT-US93-12144-36	Sequence 36, Appl
C 598	9.2	57.5	48	US-08-483-080A-200	Sequence 200, Appl	C 671	9.2	56.2	19	PCT-US95-07537A-36	Sequence 36, Appl
C 599	9.2	57.5	48	US-09-354-947-200	Sequence 200, Appl	C 672	9.2	56.2	19	PCT-US95-07537B-36	Sequence 36, Appl
C 600	9.2	57.5	48	PCT-US93-12388-200	Sequence 200, Appl	C 673	9.2	56.2	20	US-07-743-518-4	Sequence 4, Appl
C 601	9.2	57.5	50	US-08-530-492-55	Sequence 55, Appl	C 674	9.2	56.2	20	US-07-743-518-9	Sequence 9, Appl
C 602	9.2	57.5	50	US-08-472-194A-19	Sequence 19, Appl	C 675	9.2	56.2	20	US-07-977-480A-39	Sequence 39, Appl
C 603	9.2	57.5	50	US-08-463-903-64	Sequence 64, Appl	C 676	9.2	56.2	20	US-08-580-401-8	Sequence 8, Appl
C 604	9.2	57.5	50	US-08-463-903-65	Sequence 65, Appl	C 677	9.2	56.2	20	US-08-294-424-4	Sequence 4, Appl
C 605	9.2	57.5	50	US-09-262-142-19	Sequence 19, Appl	C 678	9.2	56.2	20	US-08-468-551-1	Sequence 1, Appl
C 606	9.2	57.5	50	US-08-906-517-55	Sequence 55, Appl	C 679	9.2	56.2	20	US-08-256-426B-39	Sequence 39, Appl
C 607	9.2	57.5	50	US-09-282-147-43	Sequence 43, Appl	C 680	9.2	56.2	20	US-09-166-203-44	Sequence 44, Appl
C 608	9.2	57.5	50	US-08-849-567A-19	Sequence 19, Appl	C 681	9.2	56.2	20	US-09-166-203-51	Sequence 51, Appl
C 609	9.2	57.5	50	US-07-935-695-64	Sequence 64, Appl	C 682	9.2	56.2	20	US-09-280-799-83	Sequence 83, Appl
C 610	9.2	57.5	50	US-07-935-695-65	Sequence 65, Appl	C 683	9.2	56.2	20	US-09-488-671-47	Sequence 47, Appl
C 611	9.2	57.5	50	US-08-961-309-33	Sequence 33, Appl	C 684	9.2	56.2	20	US-09-560-594-49	Sequence 49, Appl

C 685	9	56.2	20	3	US-09-377-309-44	Sequence 44, Appl	C 758	9	56.2	27	2	US-08-634-224-6	Sequence 6, Appl
C 686	9	56.2	20	3	US-09-377-309-51	Sequence 51, Appl	C 759	9	56.2	27	2	US-08-232-081B-32	Sequence 32, Appl
C 687	9	56.2	20	4	US-09-398-179-18	Sequence 18, Appl	C 760	9	56.2	27	2	US-08-634-400-6	Sequence 6, Appl
C 688	9	56.2	20	4	US-09-488-074-13	Sequence 13, Appl	C 761	9	56.2	27	2	US-08-635-878-6	Sequence 6, Appl
C 689	9	56.2	20	4	US-09-417-822-11	Sequence 11, Appl	C 762	9	56.2	27	2	US-08-770-057-6	Sequence 6, Appl
C 690	9	56.2	20	4	US-09-657-346A-33	Sequence 33, Appl	C 763	9	56.2	27	3	US-08-803-085-33	Sequence 33, Appl
C 691	9	56.2	20	4	US-09-423-978-3992	Sequence 3992, Ap	C 764	9	56.2	27	3	US-08-354-679C-7	Sequence 7, Appl
C 692	9	56.2	20	4	US-09-920-759-87	Sequence 87, Appl	C 765	9	56.2	27	3	US-08-523-894-59	Sequence 59, Appl
C 693	9	56.2	20	4	US-09-198-452A-2574	Sequence 2574, Ap	C 766	9	56.2	27	3	US-09-335-697B-6	Sequence 6, Appl
C 694	9	56.2	20	4	US-09-198-452A-6492	Sequence 6492, Ap	C 767	9	56.2	27	3	US-08-393-272B-7	Sequence 7, Appl
C 695	9	56.2	20	4	US-09-198-452A-6353	Sequence 6635, Ap	C 768	9	56.2	27	4	US-08-443-580F-7	Sequence 7, Appl
C 696	9	56.2	21	1	US-07-725-076B-2	Sequence 2, Appl	C 769	9	56.2	27	4	US-09-335-697B-6	Sequence 6, Appl
C 697	9	56.2	21	1	US-08-271-874-2	Sequence 20, Appl	C 770	9	56.2	27	4	US-08-571-263-7	Sequence 7, Appl
C 698	9	56.2	21	2	US-08-809-267-20	Sequence 20, Appl	C 771	9	56.2	27	4	US-09-142-593-35	Sequence 35, Appl
C 699	9	56.2	21	2	US-08-809-267-21	Sequence 21, Appl	C 772	9	56.2	27	4	PCT-US93-08157-7	Sequence 7, Appl
C 700	9	56.2	21	2	US-08-557-614-8	Sequence 9, Appl	C 773	9	56.2	27	5	US-08-495-743-36	Sequence 36, Appl
C 701	9	56.2	21	4	US-09-101-307D-9	Sequence 41, Appl	C 774	9	56.2	28	1	US-08-495-739-36	Sequence 36, Appl
C 702	9	56.2	21	5	US-09-394-455-41	Sequence 20, Appl	C 775	9	56.2	28	1	US-08-495-741-36	Sequence 9, Appl
C 703	9	56.2	21	5	PCT-US95-13662A-20	Sequence 21, Appl	C 776	9	56.2	28	3	US-08-911-434A-9	Sequence 36, Appl
C 704	9	56.2	21	5	PCT-US95-13662A-21	Sequence 17, Appl	C 777	9	56.2	28	4	US-08-062-023-36	Sequence 20, Appl
C 705	9	56.2	22	2	US-08-564-090A-17	Sequence 101, App	C 778	9	56.2	28	4	US-09-020-846-20	Sequence 40, Appl
C 706	9	56.2	22	2	US-09-103-875-101	Sequence 78, Appl	C 779	9	56.2	28	4	US-09-537-168-40	Sequence 21, Appl
C 707	9	56.2	22	3	US-09-302-681-78	Sequence 17, Appl	C 780	9	56.2	28	4	US-09-438-954-21	Sequence 26, Appl
C 708	9	56.2	22	5	PCT-US94-06698-17	Sequence 17, Appl	C 781	9	56.2	29	1	US-08-217-210B-26	Sequence 46, Appl
C 709	9	56.2	22	5	US-08-839-306-5	Sequence 5, Appl	C 782	9	56.2	29	3	US-08-933-983-46	Sequence 2, Appl
C 710	9	56.2	23	2	US-08-978-454-5	Sequence 5, Appl	C 783	9	56.2	29	4	US-09-304-232-853	Sequence 853, App
C 711	9	56.2	23	3	US-09-385-288-5	Sequence 39, App	C 784	9	56.2	30	1	US-08-160-670A-39	Sequence 19, Appl
C 712	9	56.2	23	4	US-09-527-030C-39	Sequence 46, Appl	C 785	9	56.2	30	1	US-08-057-167-19	Sequence 43, Appl
C 713	9	56.2	23	4	US-09-513-458-42	Sequence 43, Appl	C 786	9	56.2	30	1	US-08-229-781-43	Sequence 9, Appl
C 714	9	56.2	24	4	US-07-994-469A-46	Sequence 33, Appl	C 787	9	56.2	30	1	US-08-384-708A-9	Sequence 3, Appl
C 715	9	56.2	24	4	US-08-933-983-33	Sequence 11, Appl	C 788	9	56.2	30	1	US-08-630-918-43	Sequence 43, Appl
C 716	9	56.2	24	4	US-09-670-075A-11	Sequence 8, Appl	C 789	9	56.2	30	1	US-08-352-179-3	Sequence 2, Appl
C 717	9	56.2	25	1	US-08-336-132-8	Sequence 60, Appl	C 790	9	56.2	30	1	US-08-352-179-3	Sequence 3, Appl
C 718	9	56.2	25	1	US-08-664-449-60	Sequence 19, Appl	C 791	9	56.2	30	2	US-08-356-361-17	Sequence 17, Appl
C 719	9	56.2	25	1	US-08-743-130A-19	Sequence 22, Appl	C 792	9	56.2	30	2	US-08-769-697A-17	Sequence 3, Appl
C 720	9	56.2	25	3	US-08-192-946-22	Sequence 16, Appl	C 793	9	56.2	30	2	US-08-600-999-3	Sequence 55, Appl
C 721	9	56.2	25	4	US-09-417-822-16	Sequence 50, Appl	C 794	9	56.2	30	3	US-08-913-842-55	Sequence 4, Appl
C 722	9	56.2	25	4	US-08-982-285-50	Sequence 51, Appl	C 795	9	56.2	30	3	US-09-242-797-45	Sequence 9, Appl
C 723	9	56.2	25	4	US-08-982-285-51	Sequence 39, Appl	C 796	9	56.2	30	3	US-08-687-421-9	Sequence 1, Appl
C 724	9	56.2	25	4	US-09-358-856C-39	Sequence 43, Appl	C 797	9	56.2	30	4	US-09-494-252-13	Sequence 41, Appl
C 725	9	56.2	26	1	US-08-467-420A-43	Sequence 43, Appl	C 798	9	56.2	30	4	US-09-004-422-43	Sequence 85, Appl
C 726	9	56.2	26	1	US-08-470-110A-43	Sequence 43, Appl	C 800	9	56.2	30	4	US-09-052-919-53	Sequence 22, Appl
C 727	9	56.2	26	2	US-08-667-769A-43	Sequence 24, Appl	C 801	9	56.2	30	4	US-09-101-272G-85	Sequence 74, Appl
C 728	9	56.2	26	2	US-08-940-371-43	Sequence 23, Appl	C 802	9	56.2	30	4	US-07-65-873A-22	Sequence 2, Appl
C 729	9	56.2	26	2	US-08-463-081B-23	Sequence 24, Appl	C 803	9	56.2	30	4	US-09-231-899-14	Sequence 2, Appl
C 730	9	56.2	26	2	US-08-463-081B-24	Sequence 23, Appl	C 804	9	56.2	30	4	US-09-937-832-2	Sequence 2, Appl
C 731	9	56.2	26	2	US-08-461-379A-23	Sequence 24, Appl	C 805	9	56.2	31	2	PCT-US93-05412-19	Sequence 19, Appl
C 732	9	56.2	26	2	US-08-461-379A-24	Sequence 23, Appl	C 806	9	56.2	31	2	US-08-466-120-3	Sequence 3, Appl
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## ALIGNMENTS

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RESULT 1
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; Patent No. 6562570
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Scherr, Michaela
; APPLICANT: Rieger, Arthur D.
; TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-285
; CURRENT APPLICATION NUMBER: US/09/536,393
; EARLIER FILING DATE: 2000-03-28
; EARLIER APPLICATION NUMBER: 60/127,529
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme core
US-09-536-393-19

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Best Local Similarity 87.5%; Pred. No. 7.4;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. 6562570
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Scherr, Michaela
; APPLICANT: Rieger, Arthur D.
; TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-285
; CURRENT APPLICATION NUMBER: US/09/536,393

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; CURRENT FILING DATE: 2000-03-28
; EARLIER APPLICATION NUMBER: 60/127,529
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
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US-09-536-393-20

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Best Local Similarity 87.5%; Pred. No. 7.4;
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; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Puery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J631799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; EARLIER FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
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; LENGTH: 29
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
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US-09-270-140A-23

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Query Match      92.5%; Score 14.8; DB 4; Length 29;
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RESULT 4
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; APPLICANT: Todd, Alison
; APPLICANT: Puery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J631799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; EARLIER FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
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; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: N-ras codon 61, position 1
US-09-270-140A-25
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 29;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACAACA 16
         :|||||:|||||
Db      9 AGGCTAGCTACAACA 24
```

```
RESULT 5
US-09-270-140A-55
; Sequence 55, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J61799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
```

```
SEQ ID NO 55
```

```
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
```

```
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: codon 508 - mutant (CTT deletion) for Cystic
; OTHER INFORMATION: fibrosis
US-09-270-140A-55
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 30;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACAACA 16
         :|||||:|||||
Db      8 AGGCTAGCTACAACA 23
```

```
RESULT 6
US-09-253-955-5
; Sequence 5, Application US/09253955
; Patent No. 6140055
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
```

```
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; TITLE OF INVENTION: Molecules And Kits
; FILE REFERENCE: J1770SequenceListing
; CURRENT APPLICATION NUMBER: US/09/253,955
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,899
; EARLIER FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
```

```
SEQ ID NO 5
LENGTH: 31
TYPE: DNA
```

```
; ORGANISM: synthetic construct
US-09-253-955-5
```

```
Query Match          92.5%; Score 14.8; DB 3; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACAACA 16
         :|||||:|||||
Db      8 AGGCTAGCTACAACA 23
```

```
RESULT 7
US-09-637-405-5
; Sequence 5, Application US/09637405
; Patent No. 620113
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
```

```
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; TITLE OF INVENTION: Molecules And Kits
; FILE REFERENCE: J1770SequenceListing
; CURRENT APPLICATION NUMBER: US/09/637,405
; CURRENT FILING DATE: 2000-08-11
; EARLIER APPLICATION NUMBER: 09/253,955
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
```

```
SEQ ID NO 5
LENGTH: 31
TYPE: DNA
ORGANISM: synthetic construct
US-09-637-405-5
```

```
Query Match          92.5%; Score 14.8; DB 3; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACAACA 16
         :|||||:|||||
Db      8 AGGCTAGCTACAACA 23
```

```
RESULT 8
US-09-270-140A-42
; Sequence 42, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
```

```
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J61799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
```

```
SEQ ID NO 42
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
```

```
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: codon 542 - Cystic fibrosis
US-09-270-140A-42
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
DB 10 AGGCTAGCTACACGA 25

## RESULT 9

US-09-270-140A-45  
; Sequence 45, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Fuary, Alison  
; APPLICANT: Fuary, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: Jk11799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
; OTHER INFORMATION: Cystic Fibrosis Codon 542 - mutant (G to U)  
US-09-270-140A-45

Query Match 92.5%; Score 14.8; DB 4; Length 31;  
Best Local Similarity 87.5%; Pred. No. 7.9;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
DB 10 AGGCTAGCTACACGA 25

## RESULT 10

US-09-270-140A-48  
; Sequence 48, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Fuary, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: Jk11799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 48  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
; OTHER INFORMATION: Codon 551 - wildtype  
US-09-270-140A-48

Query Match 92.5%; Score 14.8; DB 4; Length 31;  
Best Local Similarity 87.5%; Pred. No. 7.9;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
DB 9 GGGCTAGCTACACGA 24

RESULT 11  
US-09-270-140A-51  
; Sequence 51, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Fuary, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: Jk11799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 51  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
; OTHER INFORMATION: Codon 51 - mutant (G to A)  
US-09-270-140A-51

Query Match 92.5%; Score 14.8; DB 4; Length 31;  
Best Local Similarity 87.5%; Pred. No. 7.9;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
DB 9 AGGCTAGCTACACGA 24

## RESULT 12

US-09-746-985B-5  
; Sequence 5, Application US/09746985B  
; Patent No. 6365724  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison V  
; APPLICANT: Fuary, Caroline J  
; APPLICANT: Cairns, Murray J  
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
; FILE REFERENCE: SequenceListing  
; CURRENT APPLICATION NUMBER: US/09/746,985B  
; CURRENT FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/076,899  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-09-746-985B-5

Query Match 92.5%; Score 14.8; DB 4; Length 31;  
Best Local Similarity 87.5%; Pred. No. 7.9;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
DB 8 AGGCTAGCTACACGA 23

## RESULT 13

US-09-270-140A-12  
; Sequence 12, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:

APPLICANT: Todd, Alison  
APPLICANT: Fuery, Caroline  
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
FILE REFERENCE: J6J1799  
CURRENT APPLICATION NUMBER: US/09/270,140A  
CURRENT FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 60/079,651  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
OTHER INFORMATION: H-ras codon 61, position 1-mutant  
US-09-270-140A-12

Query Match 92.5%; Score 14.8; DB 4; Length 32;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAAGA 16  
DB 10 GGGCTAGCTACAAGA 25

RESULT 14  
US-09-270-140A-15  
Sequence 15, Application US/09270140A  
Patent No. 6361941  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison  
APPLICANT: Fuery, Caroline  
APPLICANT: Cairns, Murray  
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
FILE REFERENCE: J6J1799  
CURRENT APPLICATION NUMBER: US/09/270,140A  
CURRENT FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 60/079,651  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
OTHER INFORMATION: H-ras codon 61  
US-09-270-140A-15

Query Match 92.5%; Score 14.8; DB 4; Length 32;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAAGA 16  
DB 12 GGGCTAGCTACAAGA 27

RESULT 15  
US-09-270-140A-19  
Sequence 19, Application US/09270140A  
Patent No. 6361941  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison  
APPLICANT: Fuery, Caroline  
APPLICANT: Cairns, Murray  
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
FILE REFERENCE: J6J1799

CURRENT APPLICATION NUMBER: US/09/270,140A  
CURRENT FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 60/079,651  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
OTHER INFORMATION: H-ras codon 61, position 3  
US-09-270-140A-19

Query Match 92.5%; Score 14.8; DB 4; Length 32;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAAGA 16  
DB 11 AGGCTAGCTACAAGA 26

RESULT 16  
US-09-270-140A-28  
Sequence 28, Application US/09270140A  
Patent No. 6361941  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison  
APPLICANT: Fuery, Caroline  
APPLICANT: Cairns, Murray  
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
FILE REFERENCE: J6J1799  
CURRENT APPLICATION NUMBER: US/09/270,140A  
CURRENT FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 60/079,651  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme  
US-09-270-140A-28

Query Match 92.5%; Score 14.8; DB 4; Length 32;  
Best Local Similarity 93.8%; Pred. No. 8;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAAGA 16  
DB 9 RGGCTAGCTACAAGA 24

RESULT 17  
US-09-270-140A-58  
Sequence 58, Application US/09270140A  
Patent No. 6361941  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison  
APPLICANT: Fuery, Caroline  
APPLICANT: Cairns, Murray  
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
FILE REFERENCE: J6J1799  
CURRENT APPLICATION NUMBER: US/09/270,140A  
CURRENT FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 60/079,651  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO 58
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
US-09-270-140A-58

Query Match          92.5%; Score 14.8; DB 4; Length 32;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
   :|||||:|||||
Db 9 GGGCTAGCTACACGA 24

RESULT 18
US-09-270-140A-9
; Sequence 9, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc41799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
US-09-270-140A-9

Query Match          92.5%; Score 14.8; DB 4; Length 34;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
   :|||||:|||||
Db 13 AGGCTAGCTACACGA 28

RESULT 19
US-09-270-140A-53
; Sequence 53, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc41799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 53
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```

; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
; OTHER INFORMATION: codon 08 - wildtype
US-09-270-140A-53

Query Match          92.5%; Score 14.8; DB 4; Length 34;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
   :|||||:|||||
Db 11 AGGCTAGCTACACGA 26

RESULT 20
US-09-270-140A-3
; Sequence 3, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc41799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
US-09-270-140A-3

Query Match          92.5%; Score 14.8; DB 4; Length 35;
Best Local Similarity 93.8%; Pred. No. 8;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
   :|||||:|||||
Db 11 RGCTAGCTACACGA 26

RESULT 21
US-09-270-140A-6
; Sequence 6, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc41799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
US-09-270-140A-6

Query Match          92.5%; Score 14.8; DB 4; Length 35;
Best Local Similarity 87.5%; Pred. No. 8;
```

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
Db 11 AGGCTAGCTACACGA 26

RESULT 22  
US-09-270-140A-31

; Sequence 31, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Puery, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: JcJ1799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for  
; OTHER INFORMATION: Codon 70 HIV-1 AZT resistant mutant  
US-09-270-140A-31

Query Match 92.5%; Score 14.8; DB 4; Length 35;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
Db 9 AGGCTAGCTACACGA 24

RESULT 23  
US-09-270-140A-39

; Sequence 39, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Puery, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: JcJ1799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for  
; OTHER INFORMATION: codon 74  
US-09-270-140A-39

Query Match 92.5%; Score 14.8; DB 4; Length 35;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
Db 8 AGGCTAGCTACACGA 23

RESULT 24  
US-09-270-140A-34

; Sequence 34, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Puery, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: JcJ1799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for  
; OTHER INFORMATION: codon 215 - mutant (C to U or A)  
US-09-270-140A-34

Query Match 92.5%; Score 14.8; DB 4; Length 38;  
Best Local Similarity 87.5%; Pred. No. 8.1;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
Db 11 AGGCTAGCTACACGA 26

RESULT 25  
US-09-270-140A-36

; Sequence 36, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Puery, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: JcJ1799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for  
; OTHER INFORMATION: codon 215 - mutant  
US-09-270-140A-36

Query Match 92.5%; Score 14.8; DB 4; Length 38;  
Best Local Similarity 87.5%; Pred. No. 8.1;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
Db 10 GGGCTAGCTACACGA 25

RESULT 26  
US-09-270-140A-91

; Sequence 91, Application US/09270140A

```
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jk1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 91
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dz1 DNzyme
US-09-270-140A-91
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Query Match          92.5%; Score 14.8; DB 4; Length 39;
Best Local Similarity 87.5%; Pred. No. 8.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RGCTAGCHACAACGA 16
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Db 8 GGGCTAGCTACAACGA 23
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RESULT 27
US-09-270-140A-94
; Sequence 94, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jk1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 94
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dz3 DNzyme
US-09-270-140A-94
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Query Match          92.5%; Score 14.8; DB 4; Length 39;
Best Local Similarity 87.5%; Pred. No. 8.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RGCTAGCHACAACGA 16
    :|||||:|||||
Db 8 AGGCTAGCTACAACGA 23
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RESULT 28
US-08-849-567A-85
; Sequence 85, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
; FILE REFERENCE: SCR1943S
; CURRENT APPLICATION NUMBER: US/08/849,567A
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; CURRENT FILING DATE: 1997-08-25
; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 85
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-85
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Query Match          92.5%; Score 14.8; DB 4; Length 47;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RGCTAGCHACAACGA 16
    :|||||:|||||
Db 11 AGGCTAGCTACAACGA 26
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RESULT 29
US-08-849-567A-87
; Sequence 87, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
; FILE REFERENCE: SCR1943S
; CURRENT APPLICATION NUMBER: US/08/849,567A
; PRIOR FILING DATE: 1997-08-25
; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 87
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-87
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Query Match          92.5%; Score 14.8; DB 4; Length 48;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RGCTAGCHACAACGA 16
    :|||||:|||||
Db 10 AGGCTAGCTACAACGA 25
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RESULT 30
US-08-849-567A-81
; Sequence 81, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
; FILE REFERENCE: SCR1943S
; CURRENT APPLICATION NUMBER: US/08/849,567A
; CURRENT FILING DATE: 1997-08-25
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; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-81

Query Match          92.5%; Score 14.8; DB 4; Length 49;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACAACA 16
Db      10 AGCTAGCTACAACA 25
      :|||||:|||||
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RESULT 31
US-09-253-955-8/c
; Sequence 8, Application US/09253955
; Patent No. 6140055
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; FILE REFERENCE: J11770SequenceListing
; CURRENT APPLICATION NUMBER: US/09/253,955
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,899
; EARLIER FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-253-955-8

Query Match          92.5%; Score 14.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACAACA 16
Db      22 AGCTAGCTACAACA 7
      :|||||:|||||
      :|||||:|||||

RESULT 32
US-09-637-405-8/c
; Sequence 8, Application US/09637405
; Patent No. 6201113
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; FILE REFERENCE: J11770SequenceListing
; CURRENT APPLICATION NUMBER: US/09/637,405
; CURRENT FILING DATE: 2000-08-11
; EARLIER APPLICATION NUMBER: 09/253,955
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-637-405-8

Query Match          92.5%; Score 14.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACAACA 16
Db      22 AGCTAGCTACAACA 7
      :|||||:|||||
      :|||||:|||||

RESULT 33
US-09-746-985B-8/c
; Sequence 8, Application US/09746985B
; Patent No. 6365724
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; FILE REFERENCE: SequenceListing
; CURRENT APPLICATION NUMBER: US/09/746,985B
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/076,899
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-746-985B-8

Query Match          92.5%; Score 14.8; DB 4; Length 50;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACAACA 16
Db      22 AGCTAGCTACAACA 7
      :|||||:|||||
      :|||||:|||||

RESULT 34
US-08-849-567A-86
; Sequence 86, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald R.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
; FILE REFERENCE: SCR19435
; CURRENT APPLICATION NUMBER: US/08/849,567A
; CURRENT FILING DATE: 1997-08-25
; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-86

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Best Local Similarity 92.5%; Score 14.8; DB 4; Length 51;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RGGCTAGCHACAACA 16
:|||||:|||||
Db 11 AGGCTAGCTACAACA 26

RESULT 35
US-09-253-955-2/c
Sequence 2, Application US/09253955
Patent No. 6140055
GENERAL INFORMATION:
APPLICANT: Todd, Allison V
APPLICANT: Fuery, Caroline J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: J1170SequenceListing
CURRENT APPLICATION NUMBER: US/09/253,955
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: 60/076,899
EARLIER FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 59
TYPE: DNA
ORGANISM: synthetic construct
US-09-253-955-2

Query Match
Best Local Similarity 92.5%; Score 14.8; DB 3; Length 59;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RGGCTAGCHACAACA 16
:|||||:|||||
Db 28 AGGCTAGCTACAACA 13

RESULT 36
US-09-637-405-2/c
Sequence 2, Application US/09637405
Patent No. 6201113
GENERAL INFORMATION:
APPLICANT: Todd, Allison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: J1170SequenceListing
CURRENT APPLICATION NUMBER: US/09/637,405
CURRENT FILING DATE: 2000-08-11
EARLIER APPLICATION NUMBER: 09/253,955
EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 59
TYPE: DNA
ORGANISM: synthetic construct
US-09-637-405-2

Query Match
Best Local Similarity 92.5%; Score 14.8; DB 3; Length 59;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RGGCTAGCHACAACA 16
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Db 28 AGGCTAGCTACAACA 13

RESULT 37
US-09-746-985B-2/c
Sequence 2, Application US/09746985B
Patent No. 6365724
GENERAL INFORMATION:
APPLICANT: Todd, Allison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: SequenceListing
CURRENT APPLICATION NUMBER: US/09/746,985B
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/076,899
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 59
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-09-746-985B-2

Query Match
Best Local Similarity 92.5%; Score 14.8; DB 4; Length 59;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RGGCTAGCHACAACA 16
:|||||:|||||
Db 28 AGGCTAGCTACAACA 13

RESULT 38
US-09-253-955-10/c
Sequence 10, Application US/09253955
Patent No. 6140055
GENERAL INFORMATION:
APPLICANT: Todd, Allison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: J1170SequenceListing
CURRENT APPLICATION NUMBER: US/09/253,955
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: 60/076,899
EARLIER FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 60
TYPE: DNA
ORGANISM: synthetic construct
US-09-253-955-10

Query Match
Best Local Similarity 92.5%; Score 14.8; DB 3; Length 60;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RGGCTAGCHACAACA 16
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Db 32 GGGCTAGCTACAACA 17

RESULT 39
US-09-637-405-10/c
Sequence 10, Application US/09637405
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Patent No. 620113  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison V  
APPLICANT: Fuery, Caroline J  
APPLICANT: Cairns, Murray J  
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
TITLE OF INVENTION: Molecules And Kits  
FILE REFERENCE: J1170SequencesList  
CURRENT APPLICATION NUMBER: US/09/637,405  
CURRENT FILING DATE: 2000-08-11  
EARLIER APPLICATION NUMBER: 09/253,955  
EARLIER FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 60  
TYPE: DNA  
ORGANISM: synthetic construct  
US-09-637-405-10

Query Match 92.5%; Score 14.8; DB 3; Length 60;  
Best Local Similarity 87.5%; Pred.No. 8.5;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCHACACGA 16  
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Db 32 GGGCTAGCTACACGA 17

RESULT 40  
US-09-270-140A-95/C  
Sequence 95, Application US/09270140A  
Patent No. 6361941  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison  
APPLICANT: Fuery, Caroline  
APPLICANT: Cairns, Murray  
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
FILE REFERENCE: J61799  
CURRENT APPLICATION NUMBER: US/09/270,140A  
CURRENT FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 60/079,651  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 95  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:3" zymogene  
OTHER INFORMATION: primer ek42D2  
US-09-270-140A-95

Query Match 92.5%; Score 14.8; DB 4; Length 60;  
Best Local Similarity 87.5%; Pred.No. 8.5;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCHACACGA 16  
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Db 32 GGGCTAGCTACACGA 17

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Job time : 47 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:47:52 ; Search time 154 Seconds  
(without alignments)  
366.209 Million cell updates/sec

Title: US-09-423-035B-122

Perfect score: 16

Sequence: 1 rggctagchacaacga 16

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Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 1462038

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/FCI\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
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- 6: /cgn2\_6/ptodata/1/pubpna/PCUIS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	92.5	16	10	US-09-877-526A-21 Sequence 21, Appl
2	14.8	92.5	16	10	US-09-866-316B-15 Sequence 15, Appl
3	14.8	92.5	16	10	US-09-864-785-3928 Sequence 3928, Ap
4	14.8	92.5	16	11	US-09-992-160-21 Sequence 21, Appl
5	14.8	92.5	16	11	US-09-730-289B-3896 Sequence 3896, Ap
6	14.8	92.5	16	11	US-09-780-533A-6679 Sequence 6679, Ap
7	14.8	92.5	16	11	US-09-877-478-6585 Sequence 6585, Ap
8	14.8	92.5	16	11	US-09-848-754A-9645 Sequence 9645, Ap
9	14.8	92.5	16	11	US-09-776-474-2991 Sequence 2991, Ap
10	14.8	92.5	16	11	US-09-930-423-4549 Sequence 4549, Ap
11	14.8	92.5	16	11	US-09-780-164-2602 Sequence 2602, Ap
12	14.8	92.5	16	11	US-09-827-395A-2617 Sequence 2617, Appl
13	14.8	92.5	16	12	US-10-366-191-14 Sequence 14, Appl
14	14.8	92.5	16	12	US-10-435-044A-19 Sequence 19, Appl
15	14.8	92.5	16	12	US-10-435-044A-20 Sequence 20, Appl

16	14.8	92.5	16	13	US-09-745-237A-4549 Sequence 4549, Ap
17	14.8	92.5	16	13	US-09-792-818-2304 Sequence 2304, Ap
18	14.8	92.5	16	13	US-10-279-401-11 Sequence 11, Appl
19	14.8	92.5	16	13	US-10-201-389A-13 Sequence 13, Appl
20	14.8	92.5	16	13	US-10-238-700-4666 Sequence 4666, Ap
21	14.8	92.5	16	13	US-10-277-494-445 Sequence 445, Ap
22	14.8	92.5	16	13	US-10-230-006-2677 Sequence 2677, Ap
23	14.8	92.5	16	13	US-10-306-472A-11 Sequence 11, Appl
24	14.8	92.5	16	15	US-10-151-116-12 Sequence 12, Appl
25	14.8	92.5	16	15	US-10-163-552-1997 Sequence 1997, Ap
26	14.8	92.5	16	15	US-10-156-506-8013 Sequence 8013, Ap
27	14.8	92.5	16	15	US-10-157-580A-170 Sequence 170, Appl
28	14.8	92.5	16	16	US-10-201-394A-13 Sequence 13, Appl
29	14.8	92.5	23	13	US-10-277-494-334 Sequence 334, Appl
30	14.8	92.5	23	13	US-10-277-494-335 Sequence 335, Appl
31	14.8	92.5	23	13	US-10-277-494-336 Sequence 336, Appl
32	14.8	92.5	23	13	US-10-277-494-337 Sequence 337, Appl
33	14.8	92.5	23	13	US-10-277-494-338 Sequence 338, Appl
34	14.8	92.5	23	13	US-10-277-494-339 Sequence 339, Appl
35	14.8	92.5	23	13	US-10-277-494-340 Sequence 340, Appl
36	14.8	92.5	23	13	US-10-277-494-341 Sequence 341, Appl
37	14.8	92.5	23	13	US-10-277-494-342 Sequence 342, Appl
38	14.8	92.5	23	13	US-10-277-494-343 Sequence 343, Appl
39	14.8	92.5	23	13	US-10-277-494-344 Sequence 344, Appl
40	14.8	92.5	23	13	US-10-277-494-345 Sequence 345, Appl
41	14.8	92.5	23	13	US-10-277-494-346 Sequence 346, Appl
42	14.8	92.5	23	13	US-10-277-494-347 Sequence 347, Appl
43	14.8	92.5	23	13	US-10-277-494-348 Sequence 348, Appl
44	14.8	92.5	23	13	US-10-277-494-349 Sequence 349, Appl
45	14.8	92.5	23	13	US-10-277-494-350 Sequence 350, Appl
46	14.8	92.5	23	13	US-10-277-494-351 Sequence 351, Appl
47	14.8	92.5	23	13	US-10-277-494-352 Sequence 352, Appl
48	14.8	92.5	23	13	US-10-277-494-353 Sequence 353, Appl
49	14.8	92.5	23	13	US-10-277-494-354 Sequence 354, Appl
50	14.8	92.5	23	13	US-10-277-494-355 Sequence 355, Appl
51	14.8	92.5	23	13	US-10-277-494-356 Sequence 356, Appl
52	14.8	92.5	23	13	US-10-277-494-357 Sequence 357, Appl
53	14.8	92.5	24	13	US-10-277-494-352 Sequence 352, Appl
54	14.8	92.5	25	13	US-10-277-494-327 Sequence 327, Appl
55	14.8	92.5	25	13	US-10-277-494-328 Sequence 328, Appl
56	14.8	92.5	25	13	US-10-277-494-329 Sequence 329, Appl
57	14.8	92.5	25	13	US-10-277-494-326 Sequence 326, Appl
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268	14.8	92.5	31	10	US-09-864-785-2231	Sequence	2231	Ap	341	14.8	92.5	31	10	US-09-864-785-2304	Sequence	2304	Ap
269	14.8	92.5	31	10	US-09-864-785-2232	Sequence	2232	Ap	342	14.8	92.5	31	10	US-09-864-785-2305	Sequence	2305	Ap
270	14.8	92.5	31	10	US-09-864-785-2233	Sequence	2233	Ap	343	14.8	92.5	31	10	US-09-864-785-2306	Sequence	2306	Ap
271	14.8	92.5	31	10	US-09-864-785-2234	Sequence	2234	Ap	344	14.8	92.5	31	10	US-09-864-785-2307	Sequence	2307	Ap
272	14.8	92.5	31	10	US-09-864-785-2235	Sequence	2235	Ap	345	14.8	92.5	31	10	US-09-864-785-2308	Sequence	2308	Ap
273	14.8	92.5	31	10	US-09-864-785-2236	Sequence	2236	Ap	346	14.8	92.5	31	10	US-09-864-785-2309	Sequence	2309	Ap
274	14.8	92.5	31	10	US-09-864-785-2237	Sequence	2237	Ap	347	14.8	92.5	31	10	US-09-864-785-2310	Sequence	2310	Ap
275	14.8	92.5	31	10	US-09-864-785-2238	Sequence	2238	Ap	348	14.8	92.5	31	10	US-09-864-785-2311	Sequence	2311	Ap
276	14.8	92.5	31	10	US-09-864-785-2239	Sequence	2239	Ap	349	14.8	92.5	31	10	US-09-864-785-2312	Sequence	2312	Ap
277	14.8	92.5	31	10	US-09-864-785-2240	Sequence	2240	Ap	350	14.8	92.5	31	10	US-09-864-785-2313	Sequence	2313	Ap
278	14.8	92.5	31	10	US-09-864-785-2241	Sequence	2241	Ap	351	14.8	92.5	31	10	US-09-864-785-2314	Sequence	2314	Ap
279	14.8	92.5	31	10	US-09-864-785-2242	Sequence	2242	Ap	352	14.8	92.5	31	10	US-09-864-785-2315	Sequence	2315	Ap
280	14.8	92.5	31	10	US-09-864-785-2243	Sequence	2243	Ap	353	14.8	92.5	31	10	US-09-864-785-2316	Sequence	2316	Ap
281	14.8	92.5	31	10	US-09-864-785-2244	Sequence	2244	Ap	354	14.8	92.5	31	10	US-09-864-785-2317	Sequence	2317	Ap
282	14.8	92.5	31	10	US-09-864-785-2245	Sequence	2245	Ap	355	14.8	92.5	31	10	US-09-864-785-2318	Sequence	2318	Ap
283	14.8	92.5	31	10	US-09-864-785-2246	Sequence	2246	Ap	356	14.8	92.5	31	10	US-09-864-785-2319	Sequence	2319	Ap
284	14.8	92.5	31	10	US-09-864-785-2247	Sequence	2247	Ap	357	14.8	92.5	31	10	US-09-864-785-2320	Sequence	2320	Ap
285	14.8	92.5	31	10	US-09-864-785-2248	Sequence	2248	Ap	358	14.8	92.5	31	10	US-09-864-785-2321	Sequence	2321	Ap
286	14.8	92.5	31	10	US-09-864-785-2249	Sequence	2249	Ap	359	14.8	92.5	31	10	US-09-864-785-2322	Sequence	2322	Ap
287	14.8	92.5	31	10	US-09-864-785-2250	Sequence	2250	Ap	360	14.8	92.5	31	10	US-09-864-785-2323	Sequence	2323	Ap
288	14.8	92.5	31	10	US-09-864-785-2251	Sequence	2251	Ap	361	14.8	92.5	31	10	US-09-864-785-2324	Sequence	2324	Ap
289	14.8	92.5	31	10	US-09-864-785-2252	Sequence	2252	Ap	362	14.8	92.5	31	10	US-09-864-785-2325	Sequence	2325	Ap
290	14.8	92.5	31	10	US-09-864-785-2253	Sequence	2253	Ap	363	14.8	92.5	31	10	US-09-864-785-2326	Sequence	2326	Ap
291	14.8	92.5	31	10	US-09-864-785-2254	Sequence	2254	Ap	364	14.8	92.5	31	10	US-09-864-785-2327	Sequence	2327	Ap
292	14.8	92.5	31	10	US-09-864-785-2255	Sequence	2255	Ap	365	14.8	92.5	31	10	US-09-864-785-2328	Sequence	2328	Ap
293	14.8	92.5	31	10	US-09-864-785-2256	Sequence	2256	Ap	366	14.8	92.5	31	10	US-09-864-785-2329	Sequence	2329	Ap
294	14.8	92.5	31	10	US-09-864-785-2257	Sequence	2257	Ap	367	14.8	92.5	31	10	US-09-864-785-2330	Sequence	2330	Ap
295	14.8	92.5	31	10	US-09-864-785-2258	Sequence	2258	Ap	368	14.8	92.5	31	10	US-09-864-785-2331	Sequence	2331	Ap
296	14.8	92.5	31	10	US-09-864-785-2259	Sequence	2259	Ap	369	14.8	92.5	31	10	US-09-864-785-2332	Sequence	2332	Ap
297	14.8	92.5	31	10	US-09-864-785-2260	Sequence	2260	Ap	370	14.8	92.5	31	10	US-09-864-785-2333	Sequence	2333	Ap
298	14.8	92.5	31	10	US-09-864-785-2261	Sequence	2261	Ap	371	14.8	92.5	31	10	US-09-864-785-2334	Sequence	2334	Ap
299	14.8	92.5	31	10	US-09-864-785-2262	Sequence	2262	Ap	372	14.8	92.5	31	10	US-09-864-785-2335	Sequence	2335	Ap
300	14.8	92.5	31	10	US-09-864-785-2263	Sequence	2263	Ap	373	14.8	92.5	31	10	US-09-864-785-2336	Sequence	2336	Ap
301	14.8	92.5	31	10	US-09-864-785-2264	Sequence	2264	Ap	374	14.8	92.5	31	10	US-09-864-785-2337	Sequence	2337	Ap
302	14.8	92.5	31	10	US-09-864-785-2265	Sequence	2265	Ap	375	14.8	92.5	31	10	US-09-864-785-2338	Sequence	2338	Ap
303	14.8	92.5	31	10	US-09-864-785-2266	Sequence	2266	Ap	376	14.8	92.5	31	10	US-09-864-785-2339	Sequence	2339	Ap
304	14.8	92.5	31	10	US-09-864-785-2267	Sequence	2267	Ap	377	14.8	92.5	31	10	US-09-864-785-2340	Sequence	2340	Ap
305	14.8	92.5	31	10	US-09-864-785-2268	Sequence	2268	Ap	378	14.8	92.5	31	10	US-09-864-785-2341	Sequence	2341	Ap
306	14.8	92.5	31	10	US-09-864-785-2269	Sequence	2269	Ap	379	14.8	92.5	31	10	US-09-864-785-2342	Sequence	2342	Ap
307	14.8	92.5	31	10	US-09-864-785-2270	Sequence	2270	Ap	380	14.8	92.5	31	10	US-09-864-785-23			





673	14.8	92.5	31	10	US-09-864-785-2636	Sequence 2636, Ap	746	14.8	92.5	31	11	US-09-730-289B-2952	Sequence 2952, Ap
674	14.8	92.5	31	10	US-09-864-785-2637	Sequence 2637, Ap	747	14.8	92.5	31	11	US-09-730-289B-2953	Sequence 2953, Ap
675	14.8	92.5	31	10	US-09-864-785-2638	Sequence 2638, Ap	748	14.8	92.5	31	11	US-09-730-289B-2954	Sequence 2954, Ap
676	14.8	92.5	31	10	US-09-864-785-2639	Sequence 2639, Ap	749	14.8	92.5	31	11	US-09-730-289B-2955	Sequence 2955, Ap
677	14.8	92.5	31	10	US-09-864-785-2640	Sequence 2640, Ap	750	14.8	92.5	31	11	US-09-730-289B-2956	Sequence 2956, Ap
678	14.8	92.5	31	10	US-09-864-785-2641	Sequence 2641, Ap	751	14.8	92.5	31	11	US-09-730-289B-2957	Sequence 2957, Ap
679	14.8	92.5	31	10	US-09-864-785-2642	Sequence 2642, Ap	752	14.8	92.5	31	11	US-09-730-289B-2958	Sequence 2958, Ap
680	14.8	92.5	31	10	US-09-864-785-2643	Sequence 2643, Ap	753	14.8	92.5	31	11	US-09-730-289B-2959	Sequence 2959, Ap
681	14.8	92.5	31	10	US-09-864-785-2644	Sequence 2644, Ap	754	14.8	92.5	31	11	US-09-730-289B-2960	Sequence 2960, Ap
682	14.8	92.5	31	10	US-09-864-785-2645	Sequence 2645, Ap	755	14.8	92.5	31	11	US-09-730-289B-2961	Sequence 2961, Ap
683	14.8	92.5	31	10	US-09-864-785-2646	Sequence 2646, Ap	756	14.8	92.5	31	11	US-09-730-289B-2962	Sequence 2962, Ap
684	14.8	92.5	31	10	US-09-864-785-2647	Sequence 2647, Ap	757	14.8	92.5	31	11	US-09-730-289B-2963	Sequence 2963, Ap
685	14.8	92.5	31	10	US-09-864-785-2648	Sequence 2648, Ap	758	14.8	92.5	31	11	US-09-730-289B-2964	Sequence 2964, Ap
686	14.8	92.5	31	10	US-09-864-785-2649	Sequence 2649, Ap	759	14.8	92.5	31	11	US-09-730-289B-2965	Sequence 2965, Ap
687	14.8	92.5	31	10	US-09-864-785-2650	Sequence 2650, Ap	760	14.8	92.5	31	11	US-09-730-289B-2966	Sequence 2966, Ap
688	14.8	92.5	31	10	US-09-864-785-2651	Sequence 2651, Ap	761	14.8	92.5	31	11	US-09-730-289B-2967	Sequence 2967, Ap
689	14.8	92.5	31	10	US-09-864-785-2652	Sequence 2652, Ap	762	14.8	92.5	31	11	US-09-730-289B-2968	Sequence 2968, Ap
690	14.8	92.5	31	10	US-09-864-785-2653	Sequence 2653, Ap	763	14.8	92.5	31	11	US-09-730-289B-2969	Sequence 2969, Ap
691	14.8	92.5	31	10	US-09-864-785-2654	Sequence 2654, Ap	764	14.8	92.5	31	11	US-09-730-289B-2970	Sequence 2970, Ap
692	14.8	92.5	31	10	US-09-864-785-2655	Sequence 2655, Ap	765	14.8	92.5	31	11	US-09-730-289B-2971	Sequence 2971, Ap
693	14.8	92.5	31	10	US-09-864-785-2656	Sequence 2656, Ap	766	14.8	92.5	31	11	US-09-730-289B-2972	Sequence 2972, Ap
694	14.8	92.5	31	10	US-09-864-785-2657	Sequence 2657, Ap	767	14.8	92.5	31	11	US-09-730-289B-2973	Sequence 2973, Ap
695	14.8	92.5	31	11	US-09-730-289B-2901	Sequence 2901, Ap	768	14.8	92.5	31	11	US-09-730-289B-2974	Sequence 2974, Ap
696	14.8	92.5	31	11	US-09-730-289B-2902	Sequence 2902, Ap	769	14.8	92.5	31	11	US-09-730-289B-2975	Sequence 2975, Ap
697	14.8	92.5	31	11	US-09-730-289B-2903	Sequence 2903, Ap	770	14.8	92.5	31	11	US-09-730-289B-2976	Sequence 2976, Ap
698	14.8	92.5	31	11	US-09-730-289B-2904	Sequence 2904, Ap	771	14.8	92.5	31	11	US-09-730-289B-2977	Sequence 2977, Ap
699	14.8	92.5	31	11	US-09-730-289B-2905	Sequence 2905, Ap	772	14.8	92.5	31	11	US-09-730-289B-2978	Sequence 2978, Ap
700	14.8	92.5	31	11	US-09-730-289B-2906	Sequence 2906, Ap	773	14.8	92.5	31	11	US-09-730-289B-2979	Sequence 2979, Ap
701	14.8	92.5	31	11	US-09-730-289B-2907	Sequence 2907, Ap	774	14.8	92.5	31	11	US-09-730-289B-2980	Sequence 2980, Ap
702	14.8	92.5	31	11	US-09-730-289B-2908	Sequence 2908, Ap	775	14.8	92.5	31	11	US-09-730-289B-2981	Sequence 2981, Ap
703	14.8	92.5	31	11	US-09-730-289B-2909	Sequence 2909, Ap	776	14.8	92.5	31	11	US-09-730-289B-2982	Sequence 2982, Ap
704	14.8	92.5	31	11	US-09-730-289B-2910	Sequence 2910, Ap	777	14.8	92.5	31	11	US-09-730-289B-2983	Sequence 2983, Ap
705	14.8	92.5	31	11	US-09-730-289B-2911	Sequence 2911, Ap	778	14.8	92.5	31	11	US-09-730-289B-2984	Sequence 2984, Ap
706	14.8	92.5	31	11	US-09-730-289B-2912	Sequence 2912, Ap	779	14.8	92.5	31	11	US-09-730-289B-2985	Sequence 2985, Ap
707	14.8	92.5	31	11	US-09-730-289B-2913	Sequence 2913, Ap	780	14.8	92.5	31	11	US-09-730-289B-2986	Sequence 2986, Ap
708	14.8	92.5	31	11	US-09-730-289B-2914	Sequence 2914, Ap	781	14.8	92.5	31	11	US-09-730-289B-2987	Sequence 2987, Ap
709	14.8	92.5	31	11	US-09-730-289B-2915	Sequence 2915, Ap	782	14.8	92.5	31	11	US-09-730-289B-2988	Sequence 2988, Ap
710	14.8	92.5	31	11	US-09-730-289B-2916	Sequence 2916, Ap	783	14.8	92.5	31	11	US-09-730-289B-2989	Sequence 2989, Ap
711	14.8	92.5	31	11	US-09-730-289B-2917	Sequence 2917, Ap	784	14.8	92.5	31	11	US-09-730-289B-2990	Sequence 2990, Ap
712	14.8	92.5	31	11	US-09-730-289B-2918	Sequence 2918, Ap	785	14.8	92.5	31	11	US-09-730-289B-2991	Sequence 2991, Ap
713	14.8	92.5	31	11	US-09-730-289B-2919	Sequence 2919, Ap	786	14.8	92.5	31	11	US-09-730-289B-2992	Sequence 2992, Ap
714	14.8	92.5	31	11	US-09-730-289B-2920	Sequence 2920, Ap	787	14.8	92.5	31	11	US-09-730-289B-2993	Sequence 2993, Ap
715	14.8	92.5	31	11	US-09-730-289B-2921	Sequence 2921, Ap	788	14.8	92.5	31	11	US-09-730-289B-2994	Sequence 2994, Ap
716	14.8	92.5	31	11	US-09-730-289B-2922	Sequence 2922, Ap	789	14.8	92.5	31	11	US-09-730-289B-2995	Sequence 2995, Ap
717	14.8	92.5	31	11	US-09-730-289B-2923	Sequence 2923, Ap	790	14.8	92.5	31	11	US-09-730-289B-2996	Sequence 2996, Ap
718	14.8	92.5	31	11	US-09-730-289B-2924	Sequence 2924, Ap	791	14.8	92.5	31	11	US-09-730-289B-2997	Sequence 2997, Ap
719	14.8	92.5	31	11	US-09-730-289B-2925	Sequence 2925, Ap	792	14.8	92.5	31	11	US-09-730-289B-2998	Sequence 2998, Ap
720	14.8	92.5	31	11	US-09-730-289B-2926	Sequence 2926, Ap	793	14.8	92.5	31	11	US-09-730-289B-2999	Sequence 2999, Ap
721	14.8	92.5	31	11	US-09-730-289B-2927	Sequence 2927, Ap	794	14.8	92.5	31	11	US-09-730-289B-3000	Sequence 3000, Ap
722	14.8	92.5	31	11	US-09-730-289B-2928	Sequence 2928, Ap	795	14.8	92.5	31	11	US-09-730-289B-3001	Sequence 3001, Ap
723	14.8	92.5	31	11	US-09-730-289B-2929	Sequence 2929, Ap	796	14.8	92.5	31	11	US-09-730-289B-3002	Sequence 3002, Ap
724	14.8	92.5	31	11	US-09-730-289B-2930	Sequence 2930, Ap	797	14.8	92.5	31	11	US-09-730-289B-3003	Sequence 3003, Ap
725	14.8	92.5	31	11	US-09-730-289B-2931	Sequence 2931, Ap	798	14.8	92.5	31	11	US-09-730-289B-3004	Sequence 3004, Ap
726	14.8	92.5	31	11	US-09-730-289B-2932	Sequence 2932, Ap	799	14.8	92.5	31	11	US-09-730-289B-3005	Sequence 3005, Ap
727	14.8	92.5	31	11	US-09-730-289B-2933	Sequence 2933, Ap	800	14.8	92.5	31	11	US-09-730-289B-3006	Sequence 3006, Ap
728	14.8	92.5	31	11	US-09-730-289B-2934	Sequence 2934, Ap	801	14.8	92.5	31	11	US-09-730-289B-3007	Sequence 3007, Ap
729	14.8	92.5	31	11	US-09-730-289B-2935	Sequence 2935, Ap	802	14.8	92.5	31	11	US-09-730-289B-3008	Sequence 3008, Ap
730	14.8	92.5	31	11	US-09-730-289B-2936	Sequence 2936, Ap	803	14.8	92.5	31	11	US-09-730-289B-3009	Sequence 3009, Ap
731	14.8	92.5	31	11	US-09-730-289B-2937	Sequence 2937, Ap	804	14.8	92.5	31	11	US-09-730-289B-3010	Sequence 3010, Ap
732	14.8	92.5	31	11	US-09-730-289B-2938	Sequence 2938, Ap	805	14.8	92.5	31	11	US-09-730-289B-3011	Sequence 3011, Ap
733	14.8	92.5	31	11	US-09-730-289B-2939	Sequence 2939, Ap	806	14.8	92.5	31	11	US-09-730-289B-3012	Sequence 3012, Ap
734	14.8	92.5	31	11	US-09-730-289B-2940	Sequence 2940, Ap	807	14.8	92.5	31	11	US-09-730-289B-3013	Sequence 3013, Ap
735	14.8	92.5	31	11	US-09-730-289B-2941	Sequence 2941, Ap	808	14.8	92.5	31	11	US-09-730-289B-3014	Sequence 3014, Ap
736	14.8	92.5	31	11	US-09-730-289B-2942	Sequence 2942, Ap	809	14.8	92.5	31	11	US-09-730-289B-3015	Sequence 3015, Ap
737	14.8	92.5	31	11	US-09-730-289B-2943	Sequence 2943, Ap	810	14.8	92.5	31	11	US-09-730-289B-3016	Sequence 3016, Ap
738	14.8	92.5	31	11	US-09-730-289B-2944	Sequence 2944, Ap	811	14.8	92.5	31	11	US-09-730-289B-3017	Sequence 3017, Ap
739	14.8	92.5	31	11	US-09-730-289B-2945	Sequence 2945, Ap	812	14.8	92.5	31	11	US-09-730-289B-3018	Sequence 3018, Ap
740	14.8	92.5	31	11	US-09-730-289B-2946	Sequence 2946, Ap	813	14.8	92.5	31	11	US-09-730-289B-3019	Sequence 3019, Ap
741	14.8	92.5	31	11	US-09-730-289B-2947	Sequence 2947, Ap	814	14.8	92.5	31	11	US-09-730-289B-3020	Sequence 3020, Ap
742	14.8	92.5	31	11	US-09-730-289B-2948	Sequence 2948, Ap	815	14.8	92.5	31	11	US-09-730-289B-3021	Sequence 3021, Ap
743	14.8	92.5	31	11	US-09-730-289B-2949	Sequence 2949, Ap	816	14.8	92.5	31	11	US-09-730-289B-3022	Sequence 3022, Ap
744	14.8	92.5	31	11	US-09-730-289B-2950	Sequence 2950, Ap	817	14.8	92.5	31	11	US-09-730-289B-3023	Sequence 3023, Ap
745	14.8	92.5	31	11	US-09-730-289B-2951	Sequence 2951, Ap	818	14.8	92.5	31	11	US-09-730-289B-3024	Sequence 3024, Ap

819	14.8	92.5	31	11	US-09-730-289B-3025	Sequence 3025, Ap	892	14.8	92.5	31	11	US-09-730-289B-3098	Sequence 3098, Ap
820	14.8	92.5	31	11	US-09-730-289B-3026	Sequence 3026, Ap	893	14.8	92.5	31	11	US-09-730-289B-3099	Sequence 3099, Ap
821	14.8	92.5	31	11	US-09-730-289B-3027	Sequence 3027, Ap	894	14.8	92.5	31	11	US-09-730-289B-3100	Sequence 3100, Ap
822	14.8	92.5	31	11	US-09-730-289B-3028	Sequence 3028, Ap	895	14.8	92.5	31	11	US-09-730-289B-3101	Sequence 3101, Ap
823	14.8	92.5	31	11	US-09-730-289B-3029	Sequence 3029, Ap	896	14.8	92.5	31	11	US-09-730-289B-3102	Sequence 3102, Ap
824	14.8	92.5	31	11	US-09-730-289B-3030	Sequence 3030, Ap	897	14.8	92.5	31	11	US-09-730-289B-3103	Sequence 3103, Ap
825	14.8	92.5	31	11	US-09-730-289B-3031	Sequence 3031, Ap	898	14.8	92.5	31	11	US-09-730-289B-3104	Sequence 3104, Ap
826	14.8	92.5	31	11	US-09-730-289B-3032	Sequence 3032, Ap	899	14.8	92.5	31	11	US-09-730-289B-3105	Sequence 3105, Ap
827	14.8	92.5	31	11	US-09-730-289B-3033	Sequence 3033, Ap	900	14.8	92.5	31	11	US-09-730-289B-3106	Sequence 3106, Ap
828	14.8	92.5	31	11	US-09-730-289B-3034	Sequence 3034, Ap	901	14.8	92.5	31	11	US-09-730-289B-3107	Sequence 3107, Ap
829	14.8	92.5	31	11	US-09-730-289B-3035	Sequence 3035, Ap	902	14.8	92.5	31	11	US-09-730-289B-3108	Sequence 3108, Ap
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831	14.8	92.5	31	11	US-09-730-289B-3037	Sequence 3037, Ap	904	14.8	92.5	31	11	US-09-730-289B-3110	Sequence 3110, Ap
832	14.8	92.5	31	11	US-09-730-289B-3038	Sequence 3038, Ap	905	14.8	92.5	31	11	US-09-730-289B-3111	Sequence 3111, Ap
833	14.8	92.5	31	11	US-09-730-289B-3039	Sequence 3039, Ap	906	14.8	92.5	31	11	US-09-730-289B-3112	Sequence 3112, Ap
834	14.8	92.5	31	11	US-09-730-289B-3040	Sequence 3040, Ap	907	14.8	92.5	31	11	US-09-730-289B-3113	Sequence 3113, Ap
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837	14.8	92.5	31	11	US-09-730-289B-3043	Sequence 3043, Ap	910	14.8	92.5	31	11	US-09-730-289B-3116	Sequence 3116, Ap
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839	14.8	92.5	31	11	US-09-730-289B-3045	Sequence 3045, Ap	912	14.8	92.5	31	11	US-09-730-289B-3118	Sequence 3118, Ap
840	14.8	92.5	31	11	US-09-730-289B-3046	Sequence 3046, Ap	913	14.8	92.5	31	11	US-09-730-289B-3119	Sequence 3119, Ap
841	14.8	92.5	31	11	US-09-730-289B-3047	Sequence 3047, Ap	914	14.8	92.5	31	11	US-09-730-289B-3120	Sequence 3120, Ap
842	14.8	92.5	31	11	US-09-730-289B-3048	Sequence 3048, Ap	915	14.8	92.5	31	11	US-09-730-289B-3121	Sequence 3121, Ap
843	14.8	92.5	31	11	US-09-730-289B-3049	Sequence 3049, Ap	916	14.8	92.5	31	11	US-09-730-289B-3122	Sequence 3122, Ap
844	14.8	92.5	31	11	US-09-730-289B-3050	Sequence 3050, Ap	917	14.8	92.5	31	11	US-09-730-289B-3123	Sequence 3123, Ap
845	14.8	92.5	31	11	US-09-730-289B-3051	Sequence 3051, Ap	918	14.8	92.5	31	11	US-09-730-289B-3124	Sequence 3124, Ap
846	14.8	92.5	31	11	US-09-730-289B-3052	Sequence 3052, Ap	919	14.8	92.5	31	11	US-09-730-289B-3125	Sequence 3125, Ap
847	14.8	92.5	31	11	US-09-730-289B-3053	Sequence 3053, Ap	920	14.8	92.5	31	11	US-09-730-289B-3126	Sequence 3126, Ap
848	14.8	92.5	31	11	US-09-730-289B-3054	Sequence 3054, Ap	921	14.8	92.5	31	11	US-09-730-289B-3127	Sequence 3127, Ap
849	14.8	92.5	31	11	US-09-730-289B-3055	Sequence 3055, Ap	922	14.8	92.5	31	11	US-09-730-289B-3128	Sequence 3128, Ap
850	14.8	92.5	31	11	US-09-730-289B-3056	Sequence 3056, Ap	923	14.8	92.5	31	11	US-09-730-289B-3129	Sequence 3129, Ap
851	14.8	92.5	31	11	US-09-730-289B-3057	Sequence 3057, Ap	924	14.8	92.5	31	11	US-09-730-289B-3130	Sequence 3130, Ap
852	14.8	92.5	31	11	US-09-730-289B-3058	Sequence 3058, Ap	925	14.8	92.5	31	11	US-09-730-289B-3131	Sequence 3131, Ap
853	14.8	92.5	31	11	US-09-730-289B-3059	Sequence 3059, Ap	926	14.8	92.5	31	11	US-09-730-289B-3132	Sequence 3132, Ap
854	14.8	92.5	31	11	US-09-730-289B-3060	Sequence 3060, Ap	927	14.8	92.5	31	11	US-09-730-289B-3133	Sequence 3133, Ap
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856	14.8	92.5	31	11	US-09-730-289B-3062	Sequence 3062, Ap	929	14.8	92.5	31	11	US-09-730-289B-3135	Sequence 3135, Ap
857	14.8	92.5	31	11	US-09-730-289B-3063	Sequence 3063, Ap	930	14.8	92.5	31	11	US-09-730-289B-3136	Sequence 3136, Ap
858	14.8	92.5	31	11	US-09-730-289B-3064	Sequence 3064, Ap	931	14.8	92.5	31	11	US-09-730-289B-3137	Sequence 3137, Ap
859	14.8	92.5	31	11	US-09-730-289B-3065	Sequence 3065, Ap	932	14.8	92.5	31	11	US-09-730-289B-3138	Sequence 3138, Ap
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863	14.8	92.5	31	11	US-09-730-289B-3069	Sequence 3069, Ap	936	14.8	92.5	31	11	US-09-730-289B-3142	Sequence 3142, Ap
864	14.8	92.5	31	11	US-09-730-289B-3070	Sequence 3070, Ap	937	14.8	92.5	31	11	US-09-730-289B-3143	Sequence 3143, Ap
865	14.8	92.5	31	11	US-09-730-289B-3071	Sequence 3071, Ap	938	14.8	92.5	31	11	US-09-730-289B-3144	Sequence 3144, Ap
866	14.8	92.5	31	11	US-09-730-289B-3072	Sequence 3072, Ap	939	14.8	92.5	31	11	US-09-730-289B-3145	Sequence 3145, Ap
867	14.8	92.5	31	11	US-09-730-289B-3073	Sequence 3073, Ap	940	14.8	92.5	31	11	US-09-730-289B-3146	Sequence 3146, Ap
868	14.8	92.5	31	11	US-09-730-289B-3074	Sequence 3074, Ap	941	14.8	92.5	31	11	US-09-730-289B-3147	Sequence 3147, Ap
869	14.8	92.5	31	11	US-09-730-289B-3075	Sequence 3075, Ap	942	14.8	92.5	31	11	US-09-730-289B-3148	Sequence 3148, Ap
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873	14.8	92.5	31	11	US-09-730-289B-3079	Sequence 3079, Ap	946	14.8	92.5	31	11	US-09-730-289B-3152	Sequence 3152, Ap
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877	14.8	92.5	31	11	US-09-730-289B-3083	Sequence 3083, Ap	950	14.8	92.5	31	11	US-09-730-289B-3156	Sequence 3156, Ap
878	14.8	92.5	31	11	US-09-730-289B-3084	Sequence 3084, Ap	951	14.8	92.5	31	11	US-09-730-289B-3157	Sequence 3157, Ap
879	14.8	92.5	31	11	US-09-730-289B-3085	Sequence 3085, Ap	952	14.8	92.5	31	11	US-09-730-289B-3158	Sequence 3158, Ap
880	14.8	92.5	31	11	US-09-730-289B-3086	Sequence 3086, Ap	953	14.8	92.5	31	11	US-09-730-289B-3159	Sequence 3159, Ap
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885	14.8	92.5	31	11	US-09-730-289B-3091	Sequence 3091, Ap	958	14.8	92.5	31	11	US-09-730-289B-3164	Sequence 3164, Ap
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995 14.8 92.5 31 11 US-09-730-289B-3201 Sequence 3201, Ap
996 14.8 92.5 31 11 US-09-730-289B-3202 Sequence 3202, Ap
997 14.8 92.5 31 11 US-09-730-289B-3203 Sequence 3203, Ap
998 14.8 92.5 31 11 US-09-730-289B-3204 Sequence 3204, Ap
999 14.8 92.5 31 11 US-09-730-289B-3205 Sequence 3205, Ap
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## ALIGNMENTS

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RESULT 1
US-09-877-526A-21
; Sequence 21, Application US/09877526A
; Patent No. US20020102568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Ueman, Naasim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haebertli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blact, Larry
; APPLICANT: Valish, Narendra
; TITLE OF INVENTION: A Process for the Detection of Nucleic Acid Using Nucleic Acid Ca
; FILE REFERENCE: MHB00-816-C (700/002)
; CURRENT APPLICATION NUMBER: US/09/877,526A
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,128
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif
US-09-877-526A-21

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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 1 RGCTAGCTACACGA 16

RESULT 2
US-09-866-316B-15
; Sequence 15, Application US/09866316B
; Patent No. US20020142980A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Thompson, Jim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Haebertli, Pete
; APPLICANT: Beligman, Leo
; APPLICANT: Karpelsky, Alex
; APPLICANT: Bellon, Lauren
; APPLICANT: Reynolds, Mark
; APPLICANT: Zwick, Michael
; APPLICANT: Jarvis, Thale
; APPLICANT: Woolf, Todd
; APPLICANT: Matulic-Adamic, Jasenka
; TITLE OF INVENTION: Nucleic Acid Molecules with No. US20020142980A1 Chemical Compos
; FILE REFERENCE: MHB00,873-H 500/004
; CURRENT APPLICATION NUMBER: US/09/866,316B
; PRIOR FILING DATE: 2002-03-05
; CURRENT APPLICATION NUMBER: US 09/103,656
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: US 60/082,404
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme Motif
US-09-866-316B-15

Query Match 92.5%; Score 14.8; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 1 RGCTAGCTACACGA 16

RESULT 3
US-09-864-785-3928
; Sequence 3928, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: 400/022 (MHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3928
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-3928

Query Match 92.5%; Score 14.8; DB 10; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
DB 1 RGGCTAGCTACACGA 16

## RESULT 4

US-09-992-160-21  
Sequence 21, Application US/09992160  
Publication No. US2003008295A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc  
APPLICANT: Usman, Naasim  
APPLICANT: McSwigen, Jim  
APPLICANT: Zimen, Shawn  
APPLICANT: Seiwert, Scott  
APPLICANT: Haebertl, Pete  
APPLICANT: Chowitra, Bharat  
APPLICANT: Blatt, Larry  
TITLE OF INVENTION: Nucleic Acid Sensor Molecules  
FILE REFERENCE: MBH00-816-D (700/004)  
CURRENT APPLICATION NUMBER: US/09/992,160  
CURRENT FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 21  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif  
US-09-992-160-21

Query Match 92.5%; Score 14.8; DB 11; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
DB 1 RGGCTAGCTACACGA 16

## RESULT 5

US-09-730-289B-3896  
Sequence 3896, Application US/09730289B  
Publication No. US20030050259A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
FILE REFERENCE: MBH00-864-A (400/006)  
CURRENT APPLICATION NUMBER: US/09/730,289B  
CURRENT FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: US 60/169,100  
PRIOR FILING DATE: 1999-12-06  
NUMBER OF SEQ ID NOS: 3897  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3896  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence  
US-09-730-289B-3896

Query Match 92.5%; Score 14.8; DB 11; Length 16;

Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
DB 1 RGGCTAGCTACACGA 16

## RESULT 6

US-09-780-533A-6679  
Sequence 6679, Application US/09780533A  
Publication No. US2003006011A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
APPLICANT: Chowitra, Bharat  
APPLICANT: Haebertl, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
FILE REFERENCE: MBH00-878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780,533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181,797  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6679  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-533A-6679

Query Match 92.5%; Score 14.8; DB 11; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
DB 1 RGGCTAGCTACACGA 16

## RESULT 7

US-09-877-478-6585  
Sequence 6585, Application US/09877478  
Publication No. US20030068301A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Diaper, Kenneth  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
APPLICANT: Morrissey, Dave  
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
FILE REFERENCE: MBH00-845-H (400/029)  
CURRENT APPLICATION NUMBER: US/09/877,478  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: US 07/882,712  
PRIOR FILING DATE: 1992-05-14  
PRIOR APPLICATION NUMBER: US 09/531,025  
PRIOR FILING DATE: 2000-03-20  
PRIOR APPLICATION NUMBER: US 09/636,385  
PRIOR FILING DATE: 2000-08-09  
PRIOR APPLICATION NUMBER: US 09/696,347  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 08/193,627  
PRIOR FILING DATE: 1994-02-07  
PRIOR APPLICATION NUMBER: US 08/433,993  
PRIOR FILING DATE: 1995-05-04  
PRIOR APPLICATION NUMBER: US 08/434,504  
PRIOR FILING DATE: 1995-05-04  
PRIOR APPLICATION NUMBER: US 09/436,430  
PRIOR FILING DATE: 1999-11-08

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; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6585
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-6585

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
        |||||:|||||
Db      1 RGGCTAGCTACACGA 16

RESULT 8
US-09-848-754A-9645
; Sequence 9645, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9645
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme Motif
US-09-848-754A-9645

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
        |||||:|||||
Db      1 RGGCTAGCTACACGA 16

RESULT 9
US-09-776-474-2991
; Sequence 2991, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boober, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Faltaeay, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2991
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-2991

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
        |||||:|||||
Db      1 RGGCTAGCTACACGA 16

RESULT 10
US-09-930-423-4549
; Sequence 4549, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4549
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-4549

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
        |||||:|||||
Db      1 RGGCTAGCTACACGA 16

RESULT 11
US-09-780-164-2602
; Sequence 2602, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2602
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-164-2602

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
```

Db 1 RGGCTAGCTACACGA 16

RESULT 12  
US-09-827-395A-2617  
; Sequence 2617, Application US/09827395A  
; Publication No. US20030113891A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Lawrence Blact  
; APPLICANT: James McSwiggen  
; APPLICANT: Bharat Chowitra  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor C  
; FILE REFERENCE: M8180-878-C (400/017)  
; CURRENT APPLICATION NUMBER: US/09/827,395A  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/780,533  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 2617  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2617  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Definition of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-827-395A-2617

Query Match 92.5%; Score 14.8; DB 11; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 13  
US-10-366-191-14  
; Sequence 14, Application US/10366191  
; Publication No. US20030228590A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Susan, Radka  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Haeblerli, Peter  
; TITLE OF INVENTION: Antibodies Having Specificity for Nucleic Acids  
; FILE REFERENCE: 02-030-A (900/047)  
; CURRENT APPLICATION NUMBER: US/10/366,191  
; CURRENT FILING DATE: 2003-02-12  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-366-191-14

Query Match 92.5%; Score 14.8; DB 12; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 14

US-10-435-044A-19  
; Sequence 19, Application US/10435044A  
; Publication No. US20030228615A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossi, John J  
; APPLICANT: Scherr, Michaela  
; APPLICANT: Riggs, Arthur D  
; TITLE OF INVENTION: Method For Identifying Accessible Binding Sites on RNA  
; FILE REFERENCE: 1954-2851  
; CURRENT APPLICATION NUMBER: US/10/435,044A  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: US 09/536,393  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/127,529  
; PRIOR FILING DATE: 1999-04-02  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: catalytic core  
US-10-435-044A-19

Query Match 92.5%; Score 14.8; DB 12; Length 16;  
Best Local Similarity 87.5%; Pred. No. 54;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
Db 1 AGGCTAGCTACACGA 16

RESULT 15  
US-10-435-044A-20  
; Sequence 20, Application US/10435044A  
; Publication No. US20030228615A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossi, John J  
; APPLICANT: Scherr, Michaela  
; APPLICANT: Riggs, Arthur D  
; TITLE OF INVENTION: Method For Identifying Accessible Binding Sites on RNA  
; FILE REFERENCE: 1954-2851  
; CURRENT APPLICATION NUMBER: US/10/435,044A  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: US 09/536,393  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/127,529  
; PRIOR FILING DATE: 1999-04-02  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: catalytic core  
US-10-435-044A-20

Query Match 92.5%; Score 14.8; DB 12; Length 16;  
Best Local Similarity 87.5%; Pred. No. 54;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
Db 1 GGGCTAGCTACACGA 16

RESULT 16  
US-09-745-237A-4549  
; Sequence 4549, Application US/09745237A  
; Publication No. US20030143708A1

```
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBH00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4549
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence
US-09-745-237A-4549

Query Match          92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 17
US-09-792-818-2304
Sequence 2304, Application US/09792818
Publication No. US20030134806A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Grp-2-related with Inse
FILE REFERENCE: MBH00-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2304
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-792-818-2304

Query Match          92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 18
US-10-279-401-11
Sequence 11, Application US/10279401
Publication No. US20030140362A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Macejak, Dennis
APPLICANT: Lee, Patricia
TITLE OF INVENTION: In Vivo Models For Screening Inhibitors of Hepatitis B Virus
FILE REFERENCE: 400/066 (MBH01-1336-B)
CURRENT APPLICATION NUMBER: US/10/279,401
```

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CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme Motif
US-10-279-401-11

Query Match          92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 19
US-10-201-389A-13
Sequence 13, Application US/10201389A
Publication No. US20030148928A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: Azharyev, Alex
APPLICANT: Azharyeva, Elena
APPLICANT: Antopol'sky, Maxim
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID PEPTIDE CONJUGATES
FILE REFERENCE: 600/023
CURRENT APPLICATION NUMBER: US/10/201,389A
CURRENT FILING DATE: 2002-07-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme motif
US-10-201-389A-13

Query Match          92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 20
US-10-238-700-4666
Sequence 4666, Application US/10238700
Publication No. US20030153521A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
FILE REFERENCE: 400/057 (MBH01-1158-A)
CURRENT APPLICATION NUMBER: US/10/238,700
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471
```

PRIOR FILING DATE: 2001-09-10  
NUMBER OF SEQ ID NOS: 4666  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4666  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-238-700-4666

Query Match 92.5%; Score 14.8; DB 13; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16  
DB 1 RGCTAGCTACACGA 16

RESULT 21  
US-10-277-494-445  
Sequence 445, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: MCSwigen, Jim  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MBH00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 445  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Loop Nucleic Acid Sequence  
US-10-277-494-445

Query Match 92.5%; Score 14.8; DB 13; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16  
DB 1 RGCTAGCTACACGA 16

RESULT 22  
US-10-230-006-2677  
Sequence 2677, Application US/10230006  
Publication No. US20030191077A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Fosnaugh, Kathy  
APPLICANT: MCSwigen, Jim  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI  
FILE REFERENCE: 400/056 (MBH01-1110)  
CURRENT APPLICATION NUMBER: US/10/230,006  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: US 60/315,315  
PRIOR FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 2678  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2677  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-10-230-006-2677

Query Match 92.5%; Score 14.8; DB 13; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16  
DB 1 RGCTAGCTACACGA 16

RESULT 23  
US-10-306-747A-11  
Sequence 11, Application US/10306747A  
Publication No. US20030216335A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Sandberg, Jennifer  
APPLICANT: Pavco, Pam  
APPLICANT: Gordon, Glad M.D.  
TITLE OF INVENTION: Method and Reagent for the Modulation of Female Reproductive Dise  
FILE REFERENCE: 01-1735-A (400/070)  
CURRENT APPLICATION NUMBER: US/10/306,747A  
CURRENT FILING DATE: 2002-11-27  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-306-747A-11

Query Match 92.5%; Score 14.8; DB 13; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16  
DB 1 RGCTAGCTACACGA 16

RESULT 24  
US-10-151-116-12  
Sequence 12, Application US/10151116  
Publication No. US20030104985A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Matulic-Adamic, Jasenka  
APPLICANT: Beigelman, Leo  
TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery  
FILE REFERENCE: MBH 01,639-B (600/020)  
CURRENT APPLICATION NUMBER: US/10/151,116  
CURRENT FILING DATE: 2002-05-17  
PRIOR APPLICATION NUMBER: 60/362,016  
PRIOR FILING DATE: 2002-03-06  
PRIOR APPLICATION NUMBER: 60/292,217  
PRIOR FILING DATE: 2001-05-18  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 12  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNzyme motif  
US-10-151-116-12

Query Match 92.5%; Score 14.8; DB 15; Length 16;  
Best Local Similarity 93.8%; Pred. No. 54;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
 1 RGGCTAGCTACACGA 16

## RESULT 25

US-10-163-552-1997  
 Sequence 1997, Application US/10163552  
 Publication No. US20030105051A1

## GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: McSwiggen, Jim  
 TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level  
 TITLE OF INVENTION: HER2  
 FILE REFERENCE: MBH01-1653-A (400/014)  
 CURRENT APPLICATION NUMBER: US/10/163,552  
 CURRENT FILING DATE: 2002-06-06  
 NUMBER OF SEQ ID NOS: 1997  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 1997  
 LENGTH: 16  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Substrate Sequence  
 US-10-163-552-1997

Query Match 92.5%; Score 14.8; DB 15; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 54;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
 1 RGGCTAGCTACACGA 16

## RESULT 26

US-10-156-306-8013  
 Sequence 8013, Application US/10156306  
 Publication No. US20030119017A1

## GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: McSwiggen, James  
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
 TITLE OF INVENTION: Levels of IKK-gamma and PKR  
 FILE REFERENCE: MBH01-664-A (400/050)  
 CURRENT APPLICATION NUMBER: US/10/156,306  
 CURRENT FILING DATE: 2002-05-28  
 NUMBER OF SEQ ID NOS: 8013  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 8013  
 LENGTH: 16  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Substrate sequence  
 US-10-156-306-8013

Query Match 92.5%; Score 14.8; DB 15; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 54;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
 1 RGGCTAGCTACACGA 16

## RESULT 27

US-10-157-580A-170  
 Sequence 170, Application US/10157580A  
 Publication No. US20030124513A1

## GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: McSwiggen, Jim  
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions  
 TITLE OF INVENTION: Related To Levels Of HIV  
 FILE REFERENCE: MBH01-665-A (400/051)  
 CURRENT APPLICATION NUMBER: US/10/157,580A  
 CURRENT FILING DATE: 2002-08-30  
 NUMBER OF SEQ ID NOS: 170  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 170  
 LENGTH: 16  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif  
 US-10-157-580A-170

Query Match 92.5%; Score 14.8; DB 15; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 54;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
 1 RGGCTAGCTACACGA 16

## RESULT 28

US-10-201-394A-13  
 Sequence 13, Application US/10201394A  
 Publication No. US20030130186A1

## GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: Vargese, Chandra  
 APPLICANT: Adams, Jasenka  
 APPLICANT: Karpelsky, Alexander  
 APPLICANT: Beigelman, Leonid  
 APPLICANT: Blatt, Lawrence  
 TITLE OF INVENTION: CONJUGATES AND COMPOSITIONS FOR CELLULAR DELIVERY  
 FILE REFERENCE: MBH01-882-B (600/022)  
 CURRENT APPLICATION NUMBER: US/10/201,394A  
 CURRENT FILING DATE: 2002-07-22  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 13  
 LENGTH: 16  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 US-10-201-394A-13

Query Match 92.5%; Score 14.8; DB 16; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 54;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16  
 1 RGGCTAGCTACACGA 16

## RESULT 29

US-10-277-494-334  
 Sequence 334, Application US/10277494  
 Publication No. US20030186909A1

## GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: McSwiggen, Jim  
 TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level  
 TITLE OF INVENTION: Epidermal Growth Factor Receptors  
 FILE REFERENCE: MBH00-958-K (400/064)  
 CURRENT APPLICATION NUMBER: US/10/277,494  
 CURRENT FILING DATE: 2002-10-21  
 NUMBER OF SEQ ID NOS: 446

SOFTWARE: Patentin version 3.0  
SEQ ID NO 334  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-334

Query Match 92.5%; Score 14.8; DB 13; Length 23;  
Best Local Similarity 87.5%; Pred. No. 55;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16  
:|||||:|||||  
Db 4 GGCTAGCTACACGA 19

## RESULT 30

US-10-277-494-335  
Sequence 335, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MBH00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 335  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-335

Query Match 92.5%; Score 14.8; DB 13; Length 23;  
Best Local Similarity 87.5%; Pred. No. 55;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16  
:|||||:|||||  
Db 4 GGCTAGCTACACGA 19

## RESULT 31

US-10-277-494-336  
Sequence 336, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MBH00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 336  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-336

Query Match 92.5%; Score 14.8; DB 13; Length 23;  
Best Local Similarity 87.5%; Pred. No. 55;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16  
:|||||:|||||  
Db 4 GGCTAGCTACACGA 19

## RESULT 32

US-10-277-494-337  
Sequence 337, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MBH00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 337  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-337

Query Match 92.5%; Score 14.8; DB 13; Length 23;  
Best Local Similarity 87.5%; Pred. No. 55;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16  
:|||||:|||||  
Db 4 GGCTAGCTACACGA 19

## RESULT 33

US-10-277-494-338  
Sequence 338, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MBH00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 338  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-338

Query Match 92.5%; Score 14.8; DB 13; Length 23;  
Best Local Similarity 87.5%; Pred. No. 55;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16  
:|||||:|||||  
Db 4 GGCTAGCTACACGA 19

## RESULT 34

US-10-277-494-339  
Sequence 339, Application US/10277494  
Publication No. US20030186909A1

```

; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 339
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-339

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
    :|||||:|||||
Db 4 GGGCTAGCTACACGA 19

RESULT 35
US-10-277-494-340 Application US/10277494
; Sequence 340, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 340
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-340

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
    :|||||:|||||
Db 4 AGGCTAGCTACACGA 19

RESULT 36
US-10-277-494-341 Application US/10277494
; Sequence 341, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 341

; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-342

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
    :|||||:|||||
Db 4 GGGCTAGCTACACGA 19

RESULT 37
US-10-277-494-342 Application US/10277494
; Sequence 342, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 342
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-342

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
    :|||||:|||||
Db 4 GGGCTAGCTACACGA 19

RESULT 38
US-10-277-494-343 Application US/10277494
; Sequence 343, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 343
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-343

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Wed Jan 21 10:43:29 2004

OY 1 RGGCTAGCHACACGA 16  
 :|||||:|||||  
 Db 4 GGGCTAGCTACACGA 19

## RESULT 39

US-10-277-494-344  
 ; Sequence 344; Application US/10277494  
 ; Publication No. US20030186909A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
 ; TITLE OF INVENTION: Epidermal Growth Factor Receptors  
 ; FILE REFERENCE: MBHB00-958-K (400/064)  
 ; CURRENT APPLICATION NUMBER: US/10/277,494  
 ; CURRENT FILING DATE: 2002-10-21  
 ; NUMBER OF SEQ ID NOS: 446  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 344  
 ; LENGTH: 23  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
 US-10-277-494-344

Query Match 92.5%; Score 14.8; DB 13; Length 23;

Best Local Similarity 87.5%; Pred. No. 55;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
 :|||||:|||||  
 Db 4 AGGCTAGCTACACGA 19

## RESULT 40

US-10-277-494-345  
 ; Sequence 345; Application US/10277494  
 ; Publication No. US20030186909A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
 ; TITLE OF INVENTION: Epidermal Growth Factor Receptors  
 ; FILE REFERENCE: MBHB00-958-K (400/064)  
 ; CURRENT APPLICATION NUMBER: US/10/277,494  
 ; CURRENT FILING DATE: 2002-10-21  
 ; NUMBER OF SEQ ID NOS: 446  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 345  
 ; LENGTH: 23  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
 US-10-277-494-345

Query Match 92.5%; Score 14.8; DB 13; Length 23;

Best Local Similarity 87.5%; Pred. No. 55;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
 :|||||:|||||  
 Db 4 GGGCTAGCTACACGA 19

Search completed: January 21, 2004; 08:22:21  
 Job time : 155 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:26:43 : Search time 1380 Seconds  
(without alignments)  
281.791 Million cell updates/sec

Title: US-09-423-035B-122

Perfect score: 16

Sequence: 1 rggctagchacaaga 16

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 452990

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :  
1: em\_estba:\*  
2: em\_estlm:\*  
3: em\_estlm:\*  
4: em\_estlm:\*  
5: em\_estlm:\*  
6: em\_estlm:\*  
7: em\_estlm:\*  
8: em\_estlm:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estlm:\*  
16: em\_estlm:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_dln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_pro:\*  
26: em\_gss\_png:\*  
27: em\_gss\_vrt:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.2	76.2	80	14	CA798147 CAC BL 54
2	11.8	73.8	96	28	AZ431360 1M0216F14
3	11.8	73.8	100	28	AZ658330 1M0535M02
4	11.6	72.5	44	10	BG422154 602448881

5	11.6	72.5	60	29	CNS06E2T
6	11.6	72.5	67	14	CB366166
7	11.6	72.5	86	29	AT459831 T. brucei
8	11.6	72.5	88	9	AA953865
9	11.6	72.5	90	28	AZ602406
10	11.6	72.5	93	28	BH215494
11	11.6	72.5	99	10	BG695449
12	11.6	72.5	100	13	BQ625306
13	11.2	70.0	26	28	BH901408
14	11.2	70.0	34	28	AQ025306
15	11.2	70.0	49	28	BH861777
16	11.2	70.0	49	28	BH861778
17	11.2	70.0	55	9	AA142563
18	11.2	70.0	75	13	BH866082
19	11.2	70.0	77	14	CA819431
20	11.2	70.0	85	9	AA183068
21	11.2	70.0	92	28	AZ362937
22	11.2	70.0	92	29	BZ291268
23	11.2	70.0	95	13	BH867160
24	11.2	70.0	96	13	BH862306
25	11.2	70.0	100	9	AW797834
26	11.2	70.0	100	12	BM328423
27	11.2	70.0	100	13	BH861867
28	11.2	70.0	74	29	CC179318
29	11.2	70.0	79	14	U44372
30	11.2	70.0	82	9	AA594999
31	11.2	70.0	100	10	BE330980
32	10.8	67.5	50	9	AU106358
33	10.8	67.5	80	28	BZ287687
34	10.8	67.5	82	28	AZ619815
35	10.8	67.5	85	29	AL947273
36	10.8	67.5	92	14	W17739
37	10.8	67.5	94	29	BZ291056
38	10.8	67.5	95	9	AA919502
39	10.6	66.2	32	28	AZ639727
40	10.6	66.2	37	14	CB305210
41	10.6	66.2	52	14	H08942
42	10.6	66.2	52	28	BH809438
43	10.6	66.2	54	29	CC054970
44	10.6	66.2	55	9	AJ235741
45	10.6	66.2	55	28	AZ759826
46	10.6	66.2	61	9	AI857338
47	10.6	66.2	67	9	AI931601
48	10.6	66.2	67	29	AL945283
49	10.6	66.2	74	14	N98196
50	10.6	66.2	75	9	AW057152
51	10.6	66.2	76	29	BX535085
52	10.6	66.2	78	14	H73809
53	10.6	66.2	78	28	BH235148
54	10.6	66.2	79	9	AI323764
55	10.6	66.2	79	9	AI736613
56	10.6	66.2	79	29	BZ580914
57	10.6	66.2	81	28	AQ073977
58	10.6	66.2	81	28	AF219090
59	10.6	66.2	83	9	AA986517
60	10.6	66.2	88	28	BH230938
61	10.6	66.2	91	14	CB403169
62	10.6	66.2	95	9	AI461140
63	10.6	66.2	95	9	AI971673
64	10.6	66.2	95	13	BQ823860
65	10.6	66.2	95	28	AQ072923
66	10.6	66.2	95	28	AZ603988
67	10.6	66.2	95	29	TA240A04P
68	10.6	66.2	96	9	AL644741
69	10.6	66.2	96	28	AZ916132
70	10.6	66.2	98	9	AA487184
71	10.6	66.2	98	28	BH813764
72	10.6	66.2	100	13	BQ758146
73	10.6	66.2	53	14	H18867
74	10.4	65.0	70	29	CNS036W6
75	10.4	65.0	81	29	CC457634
76	10.4	65.0	81	29	CC457634
77	10.4	65.0	81	29	CC457635

AL94587 T3 end of
CB366166 ZP001-P00
AT459831 T. brucei
AA953865 on76a12.8
AZ602406 1M0421H09
BH215494 1006027C1
BG695449 NISC 1v17
BQ625306 rd27503.Y
BH901408 SALK 0790
AQ025306 EP(3)3213
BH861777 SALK 0879
BH861778 SALK 0879
AA142563 mq59b11.x
BH866082 S062E01.P
CA819431 sau78d01.
AA183068 m86e09.r
AZ362937 1M0108B18
BZ291268 SALK 1200
BH867160 S075A07.P
BH862306 S014A04.P
AW797834 CM0-UM004
BM328423 P1C1_29_B
BH861867 S007G10.P
CC179318 SALK 0678
U44372 EMU44372.A8
AA594999 nc31e06.s
BE330980 B032A05.Y
AU106358 AU106358
BZ287687 SALK 0210
AZ619815 1M0452D18
AL947273 Arabidops
W17739 mb77g02.r1
BZ291056 SALK 1123
AA919502 vz20g11.r
AZ639727 1M0501D21
CB305210 3'EST-NE1
H08942 Y193e05.r1
BH809438 KG03411-5
CC054970 SALK 0804
AJ235741 AJ235741
AZ759826 1M0552N20
AI857338 wmo2h07.x
AI931601 u17ic02.y
AI945283 Arabidops
N98196 0266c3 czap
AW057152 ca01d12.y
BX535085 Arabidops
H73809 Y813h08.s1
BH235148 MSAD F06.
AI323764 mm11h09.x
AI736613 sb31c03.y
BZ580914 3590_1_41
AQ073977 EP(3)3398
AF219090 AF219090
AA986517 ue14c08.x
BH230938 1006160A1
CB403169 OSTR002D6
AI461140 ba75f01.y
AI971673 AL971673
BQ823860 1030113D0
AQ072923 EP(2)2127
AZ603988 1M0423C08
AL481566 T. brucei
AL644741 AL644741
AZ916132 P8C1_3.a8
AL658725 AL658725
AA487184 ab21d06.s
BH813764 SALK 0652
BQ758146 Bema01_SQ
H18867 ym45h12.r1
AL663341 Tetradon
CC457634 SALK 1111
CC457635 SALK 1111

78	10.2	63.7	44	9	AI323881	ma02e08.x	151	10	62.5	52	29	BZ765391	BZ765391
C 79	10.2	63.7	45	29	AL758879	ArabiDops	C 152	10	62.5	52	29	BZ765876	BZ765876
C 80	10.2	63.7	51	28	AZ377404	1M0131B15	C 153	10	62.5	53	13	BQ382839	BQ382839
C 81	10.2	63.7	54	14	CB019050	px72e08.y	C 154	10	62.5	54	29	BZ765887	BZ765887
C 82	10.2	63.7	58	29	BX288422	ArabiDops	C 155	10	62.5	56	29	BZ663353	BZ663353
C 83	10.2	63.7	60	29	BX003940	ArabiDops	C 156	10	62.5	57	13	BQ382141	BQ382141
C 84	10.2	63.7	62	29	AL758849	ArabiDops	C 157	10	62.5	57	13	BQ382493	BQ382493
C 85	10.2	63.7	63	10	BG362029	gb50e11.y	C 158	10	62.5	57	29	BZ762555	BZ762555
C 86	10.2	63.7	63	29	AL769268	ArabiDops	C 159	10	62.5	58	9	AI453341	AI453341
C 87	10.2	63.7	64	12	BH852825	SALK_0756	C 160	10	62.5	58	9	AI453309	AI453309
C 88	10.2	63.7	67	28	BJ066489	ArabiDops	C 161	10	62.5	58	12	BI433871	BI433871
C 89	10.2	63.7	68	28	AZ659333	1M0536H07	C 162	10	62.5	58	28	AZ917758	AZ917758
C 90	10.2	63.7	73	14	H62825	yr46e04.s1	C 163	10	62.5	59	28	AZ342599	AZ342599
C 91	10.2	63.7	74	10	BF507235	4682P-18a	C 164	10	62.5	61	9	AA070413	AA070413
C 92	10.2	63.7	79	14	CB019138	px73h03.y	C 165	10	62.5	62	14	D12015	D12015
C 93	10.2	63.7	79	14	CD346390	ECESTEf01	C 166	10	62.5	64	9	AA432439	AA432439
C 94	10.2	63.7	79	28	AZ822008	2M0095G30	C 167	10	62.5	64	9	AA432439	AA432439
C 95	10.2	63.7	82	28	AZ586406	1M0392J16	C 168	10	62.5	64	9	AA432439	AA432439
C 96	10.2	63.7	82	12	BI665456	ft22h12.x	C 169	10	62.5	64	9	AA432439	AA432439
C 97	10.2	63.7	82	28	AZ800630	2M0058E14	C 170	10	62.5	64	9	AA432439	AA432439
C 98	10.2	63.7	82	29	BZ764336	SALK_1244	C 171	10	62.5	65	9	AA432439	AA432439
C 99	10.2	63.7	83	11	CNS09161	Single re	C 172	10	62.5	65	28	BI097356	BI097356
C 100	10.2	63.7	84	28	AZ946645	2M0208H05	C 173	10	62.5	65	28	BI097356	BI097356
C 101	10.2	63.7	88	29	BX001307	ArabiDops	C 174	10	62.5	66	10	BI433871	BI433871
C 102	10.2	63.7	90	9	AI937714	wp83a12.x	C 175	10	62.5	66	10	BI433871	BI433871
C 103	10.2	63.7	90	28	AZ986258	2M0268G19	C 176	10	62.5	67	9	AA771119	AA771119
C 104	10.2	63.7	90	28	BH861753	SCALK_0879	C 177	10	62.5	67	12	BI782932	BI782932
C 105	10.2	63.7	91	9	AI941365	bc12a08.y	C 178	10	62.5	68	9	AU266458	AU266458
C 106	10.2	63.7	91	29	AG224693	Lotus_jap	C 179	10	62.5	69	10	BG019208	BG019208
C 107	10.2	63.7	92	28	BH217859	1006060E0	C 180	10	62.5	69	14	D11778	D11778
C 108	10.2	63.7	93	29	BX201107	100609G00	C 181	10	62.5	69	14	D11778	D11778
C 109	10.2	63.7	93	29	BX201107	Datio rer	C 182	10	62.5	69	14	D11778	D11778
C 110	10.2	63.7	98	14	BM036418	ECESTEe42	C 183	10	62.5	69	14	D11778	D11778
C 111	10.2	63.7	98	14	CA843512	1r48a01.y	C 184	10	62.5	71	9	AM104004	AM104004
C 112	10.2	63.7	99	14	R88374	CHS-488 Sub	C 185	10	62.5	72	28	BH911226	BH911226
C 113	10.2	63.7	100	9	AV954305	AV954305	C 186	10	62.5	72	29	AI755673	AI755673
C 114	10.2	63.7	100	10	BF023697	ECESTEa52	C 187	10	62.5	72	29	BX534001	BX534001
C 115	10.2	63.7	100	28	AZ307591	1M0009H11	C 188	10	62.5	73	9	AI529827	AI529827
C 116	10.2	63.7	100	28	BH218122	100607C1	C 189	10	62.5	73	13	BQ670558	BQ670558
C 117	10.2	63.7	23	28	AZ303987	1M0003H22	C 190	10	62.5	73	13	CE277497	CE277497
C 118	10.2	63.7	38	28	AZ806182	2M0068M03	C 191	10	62.5	73	14	R46193	R46193
C 119	10.2	63.7	39	14	D74281	CELK0794F	C 192	10	62.5	73	28	AZ656975	AZ656975
C 120	10.2	63.7	46	9	AI959989	8C36B11.x	C 193	10	62.5	73	29	CNS01V43	CNS01V43
C 121	10.2	63.7	46	9	AA758346	ab65h06.s	C 194	10	62.5	74	9	AM597442	AM597442
C 122	10.2	63.7	46	9	AI789691	whish03.r	C 195	10	62.5	74	14	D21006	D21006
C 123	10.2	63.7	48	29	BX209797	Datio rer	C 196	10	62.5	74	14	W80118	W80118
C 124	10.2	63.7	49	9	AI681141	tx44d07.x	C 197	10	62.5	74	28	BH848122	BH848122
C 125	10.2	63.7	49	28	AZ586447	1M0392B22	C 198	10	62.5	74	28	BH857828	BH857828
C 126	10.2	63.7	50	9	AU103863	ArabiDops	C 199	10	62.5	76	9	AI353603	AI353603
C 127	10.2	63.7	50	9	AU103864	ArabiDops	C 200	10	62.5	77	9	AA420608	AA420608
C 128	10.2	63.7	50	9	AU103865	ArabiDops	C 201	10	62.5	79	9	AA097644	AA097644
C 129	10.2	63.7	50	9	AU103867	ArabiDops	C 202	10	62.5	79	9	AA221444	AA221444
C 130	10.2	63.7	50	9	AU103870	ArabiDops	C 203	10	62.5	79	9	AA445499	AA445499
C 131	10.2	63.7	50	9	AU103874	ArabiDops	C 204	10	62.5	79	13	BQ097930	BQ097930
C 132	10.2	63.7	50	9	AU103875	ArabiDops	C 205	10	62.5	79	28	BH852365	BH852365
C 133	10.2	63.7	50	9	AU103877	ArabiDops	C 206	10	62.5	79	28	BH852365	BH852365
C 134	10.2	63.7	50	9	AU103880	ArabiDops	C 207	10	62.5	79	29	AL757876	AL757876
C 135	10.2	63.7	50	9	AU103881	ArabiDops	C 208	10	62.5	79	29	AL757876	AL757876
C 136	10.2	63.7	50	9	AU103882	ArabiDops	C 209	10	62.5	80	9	AI371107	AI371107
C 137	10.2	63.7	50	9	AU103885	ArabiDops	C 210	10	62.5	80	10	BG447497	BG447497
C 138	10.2	63.7	50	9	AU103892	ArabiDops	C 211	10	62.5	81	14	CD487678	CD487678
C 139	10.2	63.7	50	9	AU103893	ArabiDops	C 212	10	62.5	81	28	AA026443	AA026443
C 140	10.2	63.7	50	9	AU104386	ArabiDops	C 213	10	62.5	82	10	AA754818	AA754818
C 141	10.2	63.7	50	9	AU104387	ArabiDops	C 214	10	62.5	82	10	BF228333	BF228333
C 142	10.2	63.7	50	9	AU105969	ArabiDops	C 215	10	62.5	82	13	BQ647058	BQ647058
C 143	10.2	63.7	50	9	AU107634	ArabiDops	C 216	10	62.5	82	13	BH228283	BH228283
C 144	10.2	63.7	50	14	CB218569	NISC_nb09	C 217	10	62.5	83	14	R86482	R86482
C 145	10.2	63.7	50	29	BZ766844	SALK_1379	C 218	10	62.5	84	12	BI427494	BI427494
C 146	10.2	63.7	51	28	BH225854	1006128G0	C 219	10	62.5	84	13	BQ261711	BQ261711
C 147	10.2	63.7	51	29	AL944876	ArabiDops	C 220	10	62.5	84	13	BH232390	BH232390
C 148	10.2	63.7	52	9	AI143632	qb74c03.x	C 221	10	62.5	85	9	AA773392	AA773392
C 149	10.2	63.7	52	9	AM693197	NF063B115	C 222	10	62.5	85	9	AA615657	AA615657
C 150	10.2	63.7	52	9	AA425092	zw11f11.r	C 223	10	62.5	85	9	AA466155	AA466155

C 224	10	62.5	85	14	W3866	C 297	9.8	61.3	76	13	BQ764143
C 225	10	62.5	85	28	BH234155	C 298	9.8	61.3	91	29	AA145177
C 226	10	62.5	85	28	BH810968	C 299	9.8	61.3	91	28	AZ595050
C 227	10	62.5	87	9	A1210682	C 300	9.8	61.3	92	10	BP591436
C 228	10	62.5	87	9	AV911031	C 301	9.8	61.3	93	13	BQ766868
C 229	10	62.5	87	13	BQ758477	C 302	9.8	61.3	93	14	CD537206
C 230	10	62.5	87	14	CB384688	C 303	9.8	61.3	93	13	BQ764114
C 231	10	62.5	87	28	AO072951	C 304	9.8	61.3	98	13	BQ815594
C 232	10	62.5	87	28	BH861276	C 305	9.6	60.0	25	28	AZ866918
C 233	10	62.5	87	29	AL942715	C 306	9.6	60.0	25	28	TA138040
C 234	10	62.5	88	9	AA174733	C 307	9.6	60.0	27	28	AZ827952
C 235	10	62.5	88	13	BQ097935	C 308	9.6	60.0	30	28	BH790499
C 236	10	62.5	88	29	AL941037	C 309	9.6	60.0	31	9	AU007544
C 237	10	62.5	89	10	BF013401	C 310	9.6	60.0	31	9	AU007545
C 238	10	62.5	89	28	AZ651121	C 311	9.6	60.0	32	29	BZ763820
C 239	10	62.5	89	28	AZ839180	C 312	9.6	60.0	34	9	A1308456
C 240	10	62.5	90	10	BE568667	C 313	9.6	60.0	34	9	A1762091
C 241	10	62.5	90	28	AO939864	C 314	9.6	60.0	35	29	BX293200
C 242	10	62.5	90	28	AZ933385	C 315	9.6	60.0	37	9	A1119964
C 243	10	62.5	91	12	BM061243	C 316	9.6	60.0	38	28	AZ506380
C 244	10	62.5	91	13	BX294228	C 317	9.6	60.0	39	28	AZ799576
C 245	10	62.5	92	29	BZ663548	C 318	9.6	60.0	40	29	CC055020
C 246	10	62.5	93	9	AL680424	C 319	9.6	60.0	40	29	AL754614
C 247	10	62.5	93	28	AZ433243	C 320	9.6	60.0	41	28	BH909196
C 248	10	62.5	93	28	AZ838229	C 321	9.6	60.0	43	9	A1917489
C 249	10	62.5	93	28	BH224584	C 322	9.6	60.0	43	28	AZ502070
C 250	10	62.5	93	29	BZ54386	C 323	9.6	60.0	43	28	AZ616799
C 251	10	62.5	94	9	AA420062	C 324	9.6	60.0	43	29	AL755953
C 252	10	62.5	94	9	AA435359	C 325	9.6	60.0	46	28	AZ831199
C 253	10	62.5	94	9	AA512503	C 326	9.6	60.0	48	28	AZ438804
C 254	10	62.5	94	29	AG219003	C 327	9.6	60.0	48	28	BH807268
C 255	10	62.5	94	29	DMES47254	C 328	9.6	60.0	48	29	TA84A080
C 256	10	62.5	95	12	AL883725	C 329	9.6	60.0	49	28	AZ484612
C 257	10	62.5	95	12	B1972059	C 330	9.6	60.0	49	29	BZ586070
C 258	10	62.5	95	14	CA337825	C 331	9.6	60.0	50	9	AU102833
C 259	10	62.5	95	14	T81028	C 332	9.6	60.0	50	9	AU102837
C 260	10	62.5	95	28	AZ785550	C 333	9.6	60.0	50	9	AU104296
C 261	10	62.5	95	28	BH218664	C 334	9.6	60.0	50	9	AU105637
C 262	10	62.5	95	28	BH218664	C 335	9.6	60.0	50	9	AU105640
C 263	10	62.5	95	28	BH812878	C 336	9.6	60.0	50	9	AU107549
C 264	10	62.5	96	13	BE588022	C 337	9.6	60.0	50	9	AM246460
C 265	10	62.5	96	13	BQ815521	C 338	9.6	60.0	50	28	AZ921814
C 266	10	62.5	96	28	AZ500728	C 339	9.6	60.0	52	28	AZ663620
C 267	10	62.5	96	28	AZ823238	C 340	9.6	60.0	52	29	BZ287252
C 268	10	62.5	96	28	B42033	C 341	9.6	60.0	53	9	AA166143
C 269	10	62.5	97	9	AA691488	C 342	9.6	60.0	53	9	AA166143
C 270	10	62.5	97	9	AA797348	C 343	9.6	60.0	53	9	AA102062
C 271	10	62.5	97	9	AA969570	C 344	9.6	60.0	53	29	BZ663828
C 272	10	62.5	97	9	A1581819	C 345	9.6	60.0	53	29	TA274C090
C 273	10	62.5	97	9	AM064307	C 346	9.6	60.0	54	28	AZ308458
C 274	10	62.5	97	28	AZ916331	C 347	9.6	60.0	54	29	CC033971
C 275	10	62.5	97	28	BH910232	C 348	9.6	60.0	54	29	AL756050
C 276	10	62.5	98	14	D86759	C 349	9.6	60.0	55	9	AA727100
C 277	10	62.5	99	9	AM271170	C 350	9.6	60.0	55	29	AL942758
C 278	10	62.5	99	12	B1421049	C 351	9.6	60.0	57	10	BF417690
C 279	10	62.5	99	14	CA847174	C 352	9.6	60.0	58	9	AA908619
C 280	10	62.5	99	14	CB405696	C 353	9.6	60.0	58	9	A1324804
C 281	10	62.5	99	28	AZ773743	C 354	9.6	60.0	58	9	AA511964
C 282	10	62.5	99	28	BH418153	C 355	9.6	60.0	58	29	BX288876
C 283	10	62.5	100	9	A1934888	C 356	9.6	60.0	59	10	BF713317
C 284	10	62.5	100	9	A1934888	C 357	9.6	60.0	59	14	CA909971
C 285	10	62.5	100	9	AA466564	C 358	9.6	60.0	61	10	BG561340
C 286	10	62.5	100	10	BP874679	C 359	9.6	60.0	61	10	BE533606
C 287	10	62.5	100	10	BG208347	C 360	9.6	60.0	61	12	BG967103
C 288	10	62.5	100	10	BG693567	C 361	9.6	60.0	61	28	AZ614560
C 289	10	62.5	100	10	AM860735	C 362	9.6	60.0	63	14	CB934157
C 290	10	62.5	100	10	BE231350	C 363	9.6	60.0	63	28	AZ435853
C 291	10	62.5	100	13	BH203467	C 364	9.6	60.0	63	28	BH809023
C 292	10	62.5	100	14	CA797445	C 365	9.6	60.0	63	29	BX188578
C 293	10	62.5	19	9	A1318366	C 366	9.6	60.0	64	9	A1950653
C 294	10	62.5	32	12	B1464566	C 367	9.6	60.0	64	9	AA255961
C 295	10	62.5	32	28	AZ631344	C 368	9.6	60.0	64	10	BF400388
C 296	10	62.5	55	28	AZ633311	C 369	9.6	60.0	64	10	BE638251

370	9.6	60.0	64	10	BF219646	B219646	SNVUL3CAN	443	9.6	60.0	85	29	B2765654	B2765654	SALK 1330
371	9.6	60.0	64	28	A2410022	IM018202	Arabi	444	9.6	60.0	86	5	AA711608	AA711608	u11e08.r
372	9.6	60.0	64	29	AL770431	Arabi	445	9.6	60.0	87	28	A2776480	A2776480	ZM0010E10	
373	9.6	60.0	65	9	AM691706	AM691706	NP048C03S	446	9.6	60.0	86	9	AM722677	AM722677	C4H04mm.r
374	9.6	60.0	65	13	BQ255384	AM695014	sn69601.	447	9.6	60.0	87	14	CD395316	CD395316	Gm CK1531
375	9.6	60.0	65	28	A2855735	BQ255384	sn69601.	448	9.6	60.0	88	9	AA637658	AA637658	u10f06.r
376	9.6	60.0	66	28	BH894070	BH894070	3526_1.27	449	9.6	60.0	88	12	BM397069	BM397069	5009-0-28
377	9.6	60.0	67	9	AM184727	AM184727	fj18c09.y	450	9.6	60.0	88	14	CB912348	CB912348	VDI43E08
378	9.6	60.0	67	28	A2759905	A2759905	IM053C07	451	9.6	60.0	88	28	AZ308810	AZ308810	IM0012M07
379	9.6	60.0	67	28	BH908636	BH908636	SALK 0498	452	9.6	60.0	88	28	BH228507	BH228507	1006147C1
380	9.6	60.0	68	9	AM694424	AM694424	NE076C03S	453	9.6	60.0	89	28	CA797738	CA797738	Cac BL 48
381	9.6	60.0	68	10	BG371736	BG371736	u1-R-CV0-	454	9.6	60.0	89	28	AZ385637	AZ385637	IM0144B16
382	9.6	60.0	68	14	D45764	D45764	HUMGS02974	455	9.6	60.0	89	28	AZ495357	AZ495357	IM0331F13
383	9.6	60.0	68	29	B2595255	B2595255	SALK 0863	456	9.6	60.0	90	13	BM069470	BM069470	1488A05.x
384	9.6	60.0	69	10	BG264389	BG264389	daa81D08.	457	9.6	60.0	90	12	BM069470	BM069470	1488A05.x
385	9.6	60.0	69	14	H87983	H87983	yw18d06..x1	458	9.6	60.0	90	14	D20584	D20584	UM6501559
386	9.6	60.0	69	28	A2424099	A2424099	IM0203F01	459	9.6	60.0	90	28	BH217012	BH217012	1006049E0
387	9.6	60.0	69	29	AL752981	AL752981	Arabi	460	9.6	60.0	90	29	BZ66110	BZ66110	SGT4435-5
388	9.6	60.0	70	14	W85524	W85524	mf58e04..x1	461	9.6	60.0	90	29	AL796620	AL796620	wh58f01.x
389	9.6	60.0	70	28	A2606482	A2606482	IM0428K13	462	9.6	60.0	91	9	AM722670	AM722670	c4Q03mm.r
390	9.6	60.0	70	28	A2819833	A2819833	2M0091111	463	9.6	60.0	91	9	AU259839	AU259839	0056806.P
391	9.6	60.0	70	29	AL753206	AL753206	Arabi	464	9.6	60.0	91	14	H04321	H04321	yj20e10..s1
392	9.6	60.0	71	9	AA758458	AA758458	z17a04.s	465	9.6	60.0	92	9	AM714722	AM714722	12d04ne.x
393	9.6	60.0	71	9	AA917841	AA917841	on38e04.s	466	9.6	60.0	92	9	AM722670	AM722670	c4Q03mm.r
394	9.6	60.0	71	9	AL1869405	AL1869405	tw40c01.x	467	9.6	60.0	92	13	BH873492	BH873492	0056806.P
395	9.6	60.0	71	12	B0664004	B0664004	Arabi	468	9.6	60.0	92	13	BH873492	BH873492	0056806.P
396	9.6	60.0	71	29	AL937665	AL937665	Arabi	469	9.6	60.0	92	28	AZ438999	AZ438999	IM0229H19
397	9.6	60.0	72	9	AM636306	AM636306	B145B09..w	470	9.6	60.0	92	28	AZ477507	AZ477507	IM0297H05
398	9.6	60.0	73	9	AL217742	AL217742	qh20b04.x	471	9.6	60.0	92	29	AL942617	AL942617	Arabi
399	9.6	60.0	73	9	AM251001	AM251001	2821159.3	472	9.6	60.0	92	29	CNS04UJ2	CNS04UJ2	Arabi
400	9.6	60.0	73	9	AM499126	AM499126	SMOYAFCP	473	9.6	60.0	93	10	AJ301133	AJ301133	Arabi
401	9.6	60.0	73	12	BI081709	BI081709	602879584	474	9.6	60.0	93	10	BG057626	BG057626	nab93806.
402	9.6	60.0	73	13	BH870558	BH870558	Q015B11.P	475	9.6	60.0	93	10	BG409079	BG409079	gdb89903.y
403	9.6	60.0	73	14	CB832613	CB832613	SMWMECAV	476	9.6	60.0	93	29	AL753209	AL753209	Arabi
404	9.6	60.0	74	9	AA832576	AA832576	vw43c10..x	477	9.6	60.0	93	29	AL753209	AL753209	Arabi
405	9.6	60.0	74	10	BG231381	BG231381	na141m05.	478	9.6	60.0	93	29	DME546936	DME546936	nk35a06.s
406	9.6	60.0	74	13	BH894013	BH894013	PO8SH07.P	479	9.6	60.0	94	9	AA572291	AA572291	v152f01.r
407	9.6	60.0	74	28	A2919094	A2919094	1006013H0	480	9.6	60.0	94	13	BH869084	BH869084	M125H05.P
408	9.6	60.0	74	29	BZ661992	BZ661992	SALK 0254	481	9.6	60.0	94	28	AZ307695	AZ307695	IM0096G02
409	9.6	60.0	74	29	CNS021AA	AL198667	Tetracodon	482	9.6	60.0	94	28	AZ508919	AZ508919	IM0351C11
410	9.6	60.0	75	10	BF465862	BF465862	UI-M-CG0P	483	9.6	60.0	94	28	BH169272	BH169272	SALK 0009
411	9.6	60.0	75	10	BR368978	BR368978	601221633	484	9.6	60.0	94	28	BH169272	BH169272	SALK 0009
412	9.6	60.0	75	12	BI418320	BI418320	LJNE8755e	485	9.6	60.0	94	29	BX291595	BX291595	Arabi
413	9.6	60.0	75	12	BI049481	BI049481	B049481	486	9.6	60.0	94	29	BX291595	BX291595	Arabi
414	9.6	60.0	75	14	CB218881	CB218881	NISC nb11	487	9.6	60.0	95	10	BG154716	BG154716	sadb3803.
415	9.6	60.0	76	14	CA914432	CA914432	PC8C15918	488	9.6	60.0	95	12	BI449187	BI449187	dab01a04.
416	9.6	60.0	76	29	AL753252	AL753252	Arabi	489	9.6	60.0	95	14	X85568	X85568	HS241A8ST.h
417	9.6	60.0	76	29	HS275805	HS275805	Homo sapi	490	9.6	60.0	95	29	BX234919	BX234919	Danio rer
418	9.6	60.0	77	29	AL940027	AL940027	Arabi	491	9.6	60.0	96	14	CD402353	CD402353	Gm CK2497
419	9.6	60.0	78	10	BE023116	BE023116	sm90h11.y	492	9.6	60.0	97	9	AA429118	AA429118	zw15c01.r
420	9.6	60.0	78	13	BQ820346	BQ820346	1030083H0	493	9.6	60.0	97	28	AZ565834	AZ565834	214FVAV04
421	9.6	60.0	79	9	AA657019	AA657019	vr24h01..x	494	9.6	60.0	98	9	AM596808	AM596808	gjl6h11.y
422	9.6	60.0	79	9	AA542195	AA542195	vj59a08..x	495	9.6	60.0	98	9	AM709081	AM709081	d2E06ne.x
423	9.6	60.0	79	12	BJ055360	BJ055360	B055360	496	9.6	60.0	98	28	AZ918923	AZ918923	1006013C1
424	9.6	60.0	79	14	CB367939	CB367939	TG8ESTZy93	497	9.6	60.0	98	29	AL768784	AL768784	Arabi
425	9.6	60.0	80	9	AL820251	AL820251	AL820251	498	9.6	60.0	99	14	AU244075	AU244075	Arabi
426	9.6	60.0	80	13	BH834191	BH834191	T058A11.P	499	9.6	60.0	99	14	R79054	R79054	y187h02..x1
427	9.6	60.0	80	14	CB274864	CB274864	ma174g11.	500	9.6	60.0	99	28	BH214808	BH214808	10060094G0
428	9.6	60.0	80	29	AB082648	AB082648	Drosophila	501	9.6	60.0	100	9	AI938082	AI938082	sc41g09.x
429	9.6	60.0	81	9	AI965518	AI965518	sc73b04.y	502	9.6	60.0	100	9	AM102132	AM102132	sd83f01.y
430	9.6	60.0	81	13	BH0823042	BH0823042	1030105F0	503	9.6	60.0	100	9	AA428224	AA428224	zw33e07.s
431	9.6	60.0	81	29	AL752903	AL752903	Arabi	504	9.6	60.0	100	12	BG952334	BG952334	PM4-CT056
432	9.6	60.0	82	9	AA159678	AA159678	z085d12..s	505	9.6	60.0	100	12	BI166011	BI166011	1069P17P
433	9.6	60.0	82	9	AM598481	AM598481	s144b02.y	506	9.6	60.0	100	14	CB040559	CB040559	4003552.B
434	9.6	60.0	82	9	AM598483	AM598483	s144b04.y	507	9.6	60.0	100	14	W78697	W78697	EST00021.TE
435	9.6	60.0	83	12	BJ0000334	BJ0000334	IM0281C11	508	9.6	60.0	100	14	Z20265	Z20265	HSAAABTLV.P
436	9.6	60.0	83	28	AZ468565	AZ468565	1M0281C11	509	9.6	60.0	100	29	BZ384673	BZ384673	SALK 1358
437	9.6	60.0	84	9	AI159660	AI159660	ue98c12..x	510	9.6	60.0	100	29	CC026050	CC026050	3591_1-4
438	9.6	60.0	84	9	AM722919	AM722919	c8g12nm..x	511	9.6	60.0	100	29	AL758309	AL758309	Arabi
439	9.6	60.0	84	28	BH06484	BH06484	SALK 0335	512	9.6	60.0	100	29	CNS04SKX	CNS04SKX	Tetracodon
440	9.6	60.0	85	9	AV842614	AV842614	AV842614	513	9.4	58.8	26	28	AZ588330	AZ588330	IM0396L10
441	9.6	60.0	85	10	BF785485	BF785485	602111859	514	9.4	58.8	31	9	AA181661	AA181661	zps5c05..x
442	9.6	60.0	85	12	BI250774	BI250774	602993873	515	9.4	58.8	34	9	AI131979	AI131979	uc35h10.r

516	9.4	58.8	42	10	BF527907	BF527907 602041058	589	9.4	58.8	96	10	EG261692	BG261692 602373363
C 517	9.4	58.8	42	28	BH904167	BH904167 SALK 1040	C 590	9.4	58.8	96	14	CA592488	CA592488 bsh1.pk00
C 518	9.4	58.8	45	29	CC018920	CC018920 3591_112	C 591	9.4	58.8	97	14	AI122377	AI122377 uc61d05.x
C 519	9.4	58.8	48	29	BX178275	BX178275 Danilo rer	C 592	9.4	58.8	97	28	AQ025077	AQ025077 EP(3)0409
C 520	9.4	58.8	49	28	BH904166	BH904166 SALK 1040	C 593	9.4	58.8	97	29	AL942149	AL942149 Arabidops
C 521	9.4	58.8	49	28	BH904172	BH904172 SALK 1040	C 594	9.4	58.8	98	14	CD260607	CD260607 pema009xk
C 522	9.4	58.8	49	29	B2384940	B2384940 SALK 1362	C 595	9.4	58.8	98	29	CNS03VEB	AL262028 Tetracodon
C 523	9.4	58.8	53	28	AZ625652	AZ625652 IM04F5A24	C 596	9.4	58.8	99	9	AA676894	AA676894 z165e11.s
C 524	9.4	58.8	57	9	AI973877	AI973877 bd13a08.y	C 597	9.4	58.8	99	9	AM078836	AM078836 xbl17h07.x
C 525	9.4	58.8	58	9	AA242953	AA242953 zrf65c12.r	C 598	9.4	58.8	100	6	AA812919	AA812919 Triticum
C 526	9.4	58.8	60	13	B0899083	B0899083 mai45602.	C 599	9.4	58.8	100	6	AA207795	AA207795 mva81c01.x
C 527	9.4	58.8	60	14	B0965007	B0965007 sac05c07.	C 600	9.4	58.8	100	10	BF953180	BF953180 CM3-NN118
C 528	9.4	58.8	60	14	W85304	W85304 mfs2g09.r1	C 601	9.4	58.8	100	13	B0820967	B0820967 UB17CPB02
C 529	9.4	58.8	63	9	AA785298	AA785298 g6d01a1.f	C 602	9.4	58.8	100	14	Z20729	Z20729 HSAACITM V
C 530	9.4	58.8	63	29	BX196015	BX196015 Danilo rer	C 603	9.4	58.8	100	28	BH218154	BH218154 1006077D0
C 531	9.4	58.8	64	11	CNS09MTR	CNS09MTR Single re	C 604	9.2	57.5	22	29	TA330H07Q	TA330H07Q T. brucei
C 532	9.4	58.8	64	14	CB830802	CB830802 r109e05.y	C 605	9.2	57.5	23	28	AZ785047	AZ785047 2M0028M02
C 533	9.4	58.8	65	9	AV671702	AV671702 AV671702	C 606	9.2	57.5	28	9	AI625681	AI625681 ty59c06.x
C 534	9.4	58.8	65	28	AQ025771	AQ025771 1(2)K0581	C 607	9.2	57.5	31	28	AI677827	AI677827 wc80h06.x
C 535	9.4	58.8	65	29	AL951726	AL951726 Arabidops	C 608	9.2	57.5	31	28	AZ386571	AZ386571 IM0145C09
C 536	9.4	58.8	66	13	B0581139	B0581139 man98g07.	C 609	9.2	57.5	33	29	BZ358119	BZ358119 SALK 1319
C 537	9.4	58.8	66	28	AZ537250	AZ537250 AST-ZP031	C 610	9.2	57.5	36	28	AZ836165	AZ836165 2M0130E23
C 538	9.4	58.8	67	28	AZ848671	AZ848671 2M0149F16	C 611	9.2	57.5	37	9	AA864329	AA864329 oh56f12.s
C 539	9.4	58.8	68	9	AU256518	AU256518 AU256518	C 612	9.2	57.5	37	9	AA985715	AA985715 ue13d01.y
C 540	9.4	58.8	68	11	CNS08MT6	CNS08MT6 Single re	C 613	9.2	57.5	37	9	AA238798	AA238798 mx3c01.x
C 541	9.4	58.8	68	14	CB353381	CB353381 ZP001-P00	C 614	9.2	57.5	40	9	AA196679	AA196679 zq74g06.r
C 542	9.4	58.8	68	28	BH644273	BH644273 1008043C0	C 615	9.2	57.5	40	14	W53067	W53067 md14f07.r1
C 543	9.4	58.8	70	9	AA879217	AA879217 nw85d10.s	C 616	9.2	57.5	40	29	AL953755	AL953755 Arabidops
C 544	9.4	58.8	70	14	AA953289	AA953289 o087h06.s	C 617	9.2	57.5	41	29	TA77D03Q	TA77D03Q T. brucei
C 545	9.4	58.8	70	14	CD487659	CD487659 Gm_cK424	C 618	9.2	57.5	42	28	BH630486	BH630486 1007088F1
C 546	9.4	58.8	73	28	BH789293	BH789293 SALK 0016	C 619	9.2	57.5	42	28	AZ834022	AZ834022 2M0116D04
C 547	9.4	58.8	75	12	B1909149	B1909149 603062150	C 620	9.2	57.5	43	9	AI789785	AI789785 u153g12.x
C 548	9.4	58.8	76	9	AI746553	AI746553 u108e06.x	C 621	9.2	57.5	43	28	AZ789583	AZ789583 2M0037F01
C 549	9.4	58.8	76	10	BE058589	BE058589 en18b03.y	C 622	9.2	57.5	44	28	AZ324242	AZ324242 1M0046B08
C 550	9.4	58.8	77	28	BH789294	BH789294 SALK 0016	C 623	9.2	57.5	44	29	AL764168	AL764168 Arabidops
C 551	9.4	58.8	77	29	BZ761975	BZ761975 SALK 0839	C 624	9.2	57.5	45	29	BX191644	BX191644 Danilo rer
C 552	9.4	58.8	79	9	AM646530	AM646530 cm65h09.w	C 625	9.2	57.5	46	14	H28362	H28362 y152d04.s1
C 553	9.4	58.8	80	9	AA836179	AA836179 cd21g05.s	C 626	9.2	57.5	46	28	BH635864	BH635864 1008007F0
C 554	9.4	58.8	80	11	CNS08DOA	CNS08DOA Single re	C 627	9.2	57.5	46	29	CC037245	CC037245 3591_1-86
C 555	9.4	58.8	80	13	B0861991	B0861991 S009H05 P	C 628	9.2	57.5	47	29	TA359H02Q	TA359H02Q T. brucei
C 556	9.4	58.8	81	9	AA207801	AA207801 mv81e01.r	C 629	9.2	57.5	48	28	BH907194	BH907194 SALK 0386
C 557	9.4	58.8	81	9	AV736563	AV736563 AV736563	C 630	9.2	57.5	49	13	B0899105	B0899105 mkl45S08.
C 558	9.4	58.8	82	28	AZ586406	AZ586406 IM0392J16	C 631	9.2	57.5	49	9	AIU06744	AIU06744 AU106744
C 559	9.4	58.8	82	9	AW719858	AW719858 i7e03nm.f	C 632	9.2	57.5	50	9	AIU06745	AIU06745 AU106745
C 560	9.4	58.8	83	10	BF463412	BF463412 UI-M-CG0P	C 633	9.2	57.5	50	9	AIU06748	AIU06748 AU106748
C 561	9.4	58.8	85	9	AA919104	AA919104 O184h05.s	C 634	9.2	57.5	50	9	AIU06750	AIU06750 AU106750
C 562	9.4	58.8	85	9	AL896449	AL896449 AL896449	C 635	9.2	57.5	51	14	CB053396	CB053396 NISC q114
C 563	9.4	58.8	85	12	HJ036891	HJ036891 B036891	C 636	9.2	57.5	51	28	AZ774755	AZ774755 2M0004E01
C 564	9.4	58.8	86	9	AA236075	AA236075 z805a05.r	C 637	9.2	57.5	51	14	AI203858	AI203858 qf76g06.x
C 565	9.4	58.8	86	29	DME546383	DME546383 Drosoph11	C 638	9.2	57.5	52	9	AI287257	AI287257 qv22e08.x
C 566	9.4	58.8	86	29	DME546642	DME546642 Drosoph11	C 639	9.2	57.5	52	9	CB274957	CB274957 kv73e02.y
C 567	9.4	58.8	87	14	CB353686	CB353686 ZP001-P00	C 640	9.2	57.5	53	14	CB274957	CB274957 kv73e02.y
C 568	9.4	58.8	88	9	AM064494	AM064494 SP1094 KR	C 641	9.2	57.5	53	28	BH790547	BH790547 SALK 0573
C 569	9.4	58.8	88	14	R22567	R22567 yH24a08.s1	C 642	9.2	57.5	53	29	TA305R05Q	TA305R05Q T. brucei
C 570	9.4	58.8	88	29	AG217414	AG217414 Drosoph11	C 643	9.2	57.5	54	12	B1261027	B1261027 602972214
C 571	9.4	58.8	88	9	AL781871	AL781871 AL781871	C 644	9.2	57.5	55	9	AI610009	AI610009 cf78h03.x
C 572	9.4	58.8	89	9	AA283436	AA283436 RTH191 HT	C 645	9.2	57.5	55	12	B1447971	B1447971 d4h90d02.
C 573	9.4	58.8	89	13	B0552018	B0552018 mai24g04.	C 646	9.2	57.5	55	13	B0534625	B0534625 O11G09 1n
C 574	9.4	58.8	89	29	CC033596	CC033596 3591_1 64	C 647	9.2	57.5	55	28	B45110	B45110 HS-1060-B1-
C 575	9.4	58.8	90	11	CNS09692	CNS09692 Single re	C 648	9.2	57.5	56	14	CB274974	CB274974 kv74h09.y
C 576	9.4	58.8	91	14	CB394112	CB394112 OSTRL1H4	C 649	9.2	57.5	56	28	BH652317	BH652317 SALK 0744
C 577	9.4	58.8	91	14	CD029357	CD029357 mgcW016XM	C 650	9.2	57.5	58	9	AI195289	AI195289 ue71a03.r
C 578	9.4	58.8	91	28	BH851397	BH851397 SALK 0729	C 651	9.2	57.5	58	9	AA480462	AA480462 ne70d10.s
C 579	9.4	58.8	92	28	AZ778554	AZ778554 2M0013M10	C 652	9.2	57.5	58	12	B1944424	B1944424 b6d21d05.
C 580	9.4	58.8	93	12	BI689678	BI689678 wo39g12.x	C 653	9.2	57.5	58	29	BZ380332	BZ380332 CM3-NN118
C 581	9.4	58.8	93	12	BI689678	BI689678 603316173	C 654	9.2	57.5	58	29	TA113A05Q	TA113A05Q T. brucei
C 582	9.4	58.8	93	29	AB082060	AB082060 Drosoph11	C 655	9.2	57.5	59	28	AZ487775	AZ487775 IM0317112
C 583	9.4	58.8	94	28	AL821922	AL821922 AL821922	C 656	9.2	57.5	59	28	AQ254664	AQ254664 EP(3)0887
C 584	9.4	58.8	94	28	AZ822068	AZ822068 2M0095D02	C 657	9.2	57.5	60	10	BF471331	BF471331 UI-M-BH3-
C 585	9.4	58.8	94	28	AZ827884	AZ827884 2M0104N03	C 658	9.2	57.5	60	14	CB277341	CB277341 kv64c10.y
C 586	9.4	58.8	94	29	AL755189	AL755189 Arabidops	C 659	9.2	57.5	60	28	AZ782748	AZ782748 2M0023F07
C 587	9.4	58.8	95	14	CB930289	CB930289 r193b02.y	C 660	9.2	57.5	60	29	BX232154	BX232154 Danilo rer
C 588	9.4	58.8	95	29	AL943193	AL943193 Arabidops	C 661	9.2	57.5	60	29	BX535184	BX535184 Arabidops

662	9.2	57.5	61	9	AA682677	AA682677 zj86e01.s	735	9.2	57.5	79	9	AI619804	AI619804 ty53d10.x
C 663	9.2	57.5	61	9	AI469429	AI469429 tm08g02.x	736	9.2	57.5	79	10	BF507191	BF507191 2912p-22d
C 664	9.2	57.5	61	13	BQ759608	BQ759608 EBP103.SQ	C 737	9.2	57.5	79	12	BG942642	BG942642 ax27g11.x
C 665	9.2	57.5	61	28	AZ916244	AZ916244 Psrt_4Ds	C 738	9.2	57.5	79	12	BJ059037	BJ059037 BJ059037
C 666	9.2	57.5	61	29	BZ762814	BZ762814 SALK_1058	C 739	9.2	57.5	79	29	BZ56346	BZ56346 SALK_0924
C 667	9.2	57.5	62	9	AF211691	AF211691 AF211691	C 740	9.2	57.5	80	9	AU256734	AU256734 AU256734
C 668	9.2	57.5	62	28	AZ520963	AZ520963 1006023A0	C 741	9.2	57.5	80	13	BQ822592	BQ822592 1030101H0
C 669	9.2	57.5	63	129	BZ764789	BZ764789 SALK_1269	C 742	9.2	57.5	80	13	BU743537	BU743537 ma133d10.
C 670	9.2	57.5	63	13	BQ786079	BQ786079 sag63c10.	C 743	9.2	57.5	80	14	N55635	N55635 ESTG183.Rat
C 671	9.2	57.5	63	28	BH146129	BH146129 BG01930-3	C 744	9.2	57.5	80	29	BZ748860	BZ748860 EY01909-5
C 672	9.2	57.5	64	12	BI912407	BI912407 603290867	C 745	9.2	57.5	80	29	TAG19040	TA1494432
C 673	9.2	57.5	64	14	CB277338	CB277338 kue4b09.y	C 746	9.2	57.5	81	9	AI494432	AI494432 GY99f03.x
C 674	9.2	57.5	64	28	AZ303997	AZ303997 1M00003K01	C 747	9.2	57.5	82	14	F35562	F35562 HSPD31958.H
C 675	9.2	57.5	65	9	AI526212	AI526212 w054a05.x	C 748	9.2	57.5	82	28	AZ800630	AZ800630 2M0038E14
C 676	9.2	57.5	65	14	CB274956	CB274956 ku73e01.y	C 749	9.2	57.5	82	28	BH847053	BH847053 SALK_0129
C 677	9.2	57.5	65	28	AZ921399	AZ921399 1006029G0	C 750	9.2	57.5	83	9	AI310837	AI310837 ta43a11.x
C 678	9.2	57.5	65	28	BH865885	BH865885 SALK_1000	C 751	9.2	57.5	83	13	BQ246646	BQ246646 TAB15007E
C 679	9.2	57.5	65	29	BX535185	BX535185 Arabidops	C 752	9.2	57.5	83	29	BZ383815	BZ383815 SALK_1345
C 680	9.2	57.5	66	10	BG563172	BG563172 602582083	C 753	9.2	57.5	84	9	AI318731	AI318731 a1601m.f
C 681	9.2	57.5	66	10	AZ800929	AZ800929 2M0059M10	C 754	9.2	57.5	84	10	BG700680	BG700680 602682317
C 682	9.2	57.5	66	29	AG216222	AG216222 Dicosophil	C 755	9.2	57.5	84	13	BQ274157	BQ274157 Kc47H04.Y
C 683	9.2	57.5	67	9	AA576816	AA576816 tm77g01.s	C 756	9.2	57.5	84	28	BH863008	BH863008 SALK_0929
C 684	9.2	57.5	67	28	AZ588886	AZ588886 1M0397D06	C 757	9.2	57.5	85	9	AA693766	AA693766 z147H12.s
C 685	9.2	57.5	67	29	BZ384630	BZ384630 SALK_1358	C 758	9.2	57.5	85	13	BU870526	BU870526 0013F07.P
C 686	9.2	57.5	68	9	AI593771	AI593771 vt72d09.x	C 759	9.2	57.5	85	14	T25066	T25066 EST641.Huma
C 687	9.2	57.5	68	10	BE463636	BE463636 h896c11.x	C 760	9.2	57.5	85	14	T63730	T63730 Yc16h02.r1
C 688	9.2	57.5	68	14	CB365575	CB365575 ZF001-P00	C 761	9.2	57.5	85	28	BH896791	BH896791 3526_155
C 689	9.2	57.5	68	28	AQ025753	AQ025753 1(2)k0520	C 762	9.2	57.5	86	28	AZ809289	AZ809289 2M0073A14
C 690	9.2	57.5	68	28	AZ808394	AZ808394 2M0071121	C 763	9.2	57.5	86	29	AL758982	AL758982 Arabidops
C 691	9.2	57.5	68	29	CC156334	CC156334 KST062.Ba	C 764	9.2	57.5	87	9	AM100540	AM100540 sds6e05.y
C 692	9.2	57.5	68	28	AZ783790	AZ783790 2M0025M20	C 765	9.2	57.5	87	10	BF382023	BF382023 601816344
C 693	9.2	57.5	69	28	BH905447	BH905447 SALK_1076	C 766	9.2	57.5	87	12	BI781815	BI781815 kh01903.Y
C 694	9.2	57.5	69	29	BZ357591	BZ357591 SALK_1309	C 767	9.2	57.5	87	13	BU651003	BU651003 1112090F0
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C 697	9.2	57.5	71	9	AJ239810	AJ239810 A239810	C 770	9.2	57.5	88	28	BH172590	BH172590 SALK_0059
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C 700	9.2	57.5	71	29	DB7503	DB7503 Schistocoma	C 773	9.2	57.5	89	14	CB686411	CB686411 Br01D_04h
C 701	9.2	57.5	72	10	BG259391	BG259391 602378478	C 774	9.2	57.5	89	28	AF149519	AF149519 AF149519
C 702	9.2	57.5	72	14	CB217416	CB217416 NISC.nb02	C 775	9.2	57.5	89	28	AZ921956	AZ921956 HRC02G04
C 703	9.2	57.5	72	28	AZ666486	AZ666486 1M0548108	C 776	9.2	57.5	90	14	CB384048	CB384048 TGESt.kyH5
C 704	9.2	57.5	72	28	BH632561	BH632561 1007096A0	C 777	9.2	57.5	90	28	BH216178	BH216178 1006040H1
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847	9.2	56.2	30	10	BE3561270	BE3561270	920	9	56.2	48	28	BH790348	BH790348 SALX_0568
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## ALIGNMENTS

RESULT 1 80 bp mRNA linear EST 05-DEC-2002  
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 ORGANISM Theobroma cacao  
 EST. Theobroma cacao  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 1 (bases 1 to 80)  
 Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel  
 E.R. and Jones, C.A.  
 Gene discovery and microarray analysis of cacao (Theobroma cacao  
 L.) varieties  
 Plant 216 (2), 255-264 (2002)  
 JOURNAL 22337596  
 MEDLINE 12447539  
 PUBMED

## COMMENT

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 Tel: +44 1664 416644  
 Email: Paul.Jones@eu.affem.com  
 Seg primer: 73.  
 Location/Qualifiers

## FEATURES

## source

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## BASE COUNT

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## ORIGIN

Query Match 76.2%; Score 12.2; DB 14; Length 80;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+04;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

## Qy

1 RGCGTACGACACG 15

36 GCGGTACTACTACG 50

DB

## RESULT 2

A2431360 96 bp DNA linear GSS 03-OCT-2000  
 LOCUS 1M0216F14F Mouse 10kb plasmid UGCLM library Mus musculus genomic  
 DEFINITION clone UGCLM0216F14 F, genomic survey sequence.  
 A2431360  
 ACCESSION A2431360.1 GI:10555373  
 VERSION GSS.  
 KEYWORDS Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 SOURCE Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 96)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## JOURNAL

COMMENT Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

## FEATURES

## source

1..96  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCLM0216F14"

/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UGCM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1/4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 31 a 32 c 12 g 21 t  
ORIGIN

Query Match 73.8%; Score 11.8; DB 28; Length 96;  
Best Local Similarity 84.6%; Pred. No. 2.1e+04;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

cy 1 RGGCTAGCACA 13  
:|||||:  
4 GGGCTAGCACA 16

Db

RESULT 3  
AZ658330 100 bp DNA linear GSS 14-DEC-2000  
LOCUS clone UGCM0535M02 F, genomic survey sequence.  
DEFINITION  
ACCESSION AZ658330 GI:11795476  
VERSION  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM  
MUS MUSCULUS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 100)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
COMMENT Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduw@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0535 row: M column: 02  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 100.  
Location/Qualifiers  
1. 100  
/organism="Mus musculus"  
/mol type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

/clone="UGCM0535M02"  
/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UGCM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1/4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 23 a 13 c 36 g 28 t  
ORIGIN

Query Match 73.8%; Score 11.8; DB 28; Length 100;  
Best Local Similarity 84.6%; Pred. No. 2.2e+04;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

cy 1 RGGCTAGCACA 13  
:|||||:  
5 GGGCTAGCACA 17

Db

RESULT 4  
BG422154/c 44 bp mRNA linear EST 14-MAR-2001  
LOCUS 602448881F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4587189 5', mRNA sequence.  
DEFINITION  
ACCESSION BG422154  
VERSION BG422154.1 GI:13328660  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 44)  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: DCTD/BTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.jnl.gov  
Plate: LNCM317 row: b column: 22  
High quality sequence stop: 44.  
Location/Qualifiers  
1. 44  
/organism="Homo sapiens"  
/mol type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4587189"  
/tissue\_type="renal cell adenocarcinoma"  
/lab host="DH10B (phage-resistant)"  
/clone lib="NIH MGC 14"  
/note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## BASE COUNT

6 a 10 c 21 g 7 t

Query Match 72.5%; Score 11.6; DB 10; Length 44;  
Best Local Similarity 75.0%; Pred. No. 2e+04; 2; Indels 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 2;

QY 1 RGCTAGCHACACGA 16  
39 AGCCAGCTACACGA 24

RESULT 5  
CNS06B2T 60 bp DNA linear GSS 17-JUN-2001  
LOCUS T3 end of clone AR0A018A08 of library AR0A from strain CBS 732 of  
DEFINITION Zygocaccharomyces rouxii, genomic survey sequence.

ACCESSION AL394587.1 GI:12145628  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
1 (bases 1 to 60)  
Soulciet, J., Aigle, M., Artiguenave, F., Blandin, G.,  
Bolotin-Fukuhara, M., Bon, E., Brothier, P., Casaregola, S.,  
de Montigny, J., Dujon, B., Durans, P., Leplingle, A., Lorente, B.,  
Malpertuy, A., Neugejse, C., Olier-Kalogeropoulos, O., Potier, S.,  
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,  
Wincker, P., and Weissenbach, J.  
Genomic exploration of the hemiascomycetous yeasts: 1. A set of  
Yeast species for molecular evolution studies

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
2 (bases 1 to 60)  
de Montigny, J., Straub, M., Potier, S., Tekala, F., Dujon, B.,  
Wincker, P., Artiguenave, F., and Soulciet, J.  
Genomic exploration of the hemiascomycetous yeasts: 8.  
Zygocaccharomyces rouxii

JOURNAL  
MEDLINE  
PUBMED  
20584718  
11152883  
3 (bases 1 to 60)  
Genoscope.  
Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,  
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
seq@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
This GSS is part of a random genomic sequencing program of thirteen  
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces  
exiguus, Saccharomyces servazii, Zygocaccharomyces rouxii,  
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces  
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Kluyveromyces  
angustis, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,  
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to  
5 kb were prepared and both extremities were sequenced. See  
keywords for description of this sequence and for the sequence of  
the other extremity of this insert.

COMMENT  
JOURNAL  
TITLE  
REFERENCE  
AUTHORS  
JOURNAL  
MEDLINE  
PUBMED  
20584718  
11152883  
3 (bases 1 to 60)  
Genoscope.  
Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,  
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
seq@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
This GSS is part of a random genomic sequencing program of thirteen  
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces  
exiguus, Saccharomyces servazii, Zygocaccharomyces rouxii,  
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces  
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Kluyveromyces  
angustis, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,  
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to  
5 kb were prepared and both extremities were sequenced. See  
keywords for description of this sequence and for the sequence of  
the other extremity of this insert.

## FEATURES

Location/Qualifiers  
1..60  
/organism="Zygocaccharomyces rouxii"  
/mol\_type="genomic DNA"  
/strain="CBS 732"  
/db\_xref="taxon:4956"  
/clone="AR0A018A08"

/clone lib="AR0A"  
/note="end : T3"  
BASE COUNT 17 a 25 c 11 g 6 t 1 others

Query Match 72.5%; Score 11.6; DB 29; Length 60;  
Best Local Similarity 80.0%; Pred. No. 2.3e+04;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCTAGCHACACGA 16  
7 GCCTAGCCANACGA 21

RESULT 6  
CB366166 67 bp mRNA linear EST 17-MAR-2003  
LOCUS ZF001-P00049-DPE-F2-D F10 GISZP001 Danio rerio cDNA clone  
DEFINITION IMAGE:6910149 5' similar to fp15a03.y1 zebrafish gridded kidney  
Danio rerio cDNA clone IMAGE:4729612 5' similar to WP:CE25522  
Y61A9UA.E, mRNA sequence.

ACCESSION CB366166  
VERSION CB366166.1 GI:29016477  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
1 (bases 1 to 67)  
Mathavan, S., Wei, C., Thoreau, H., Chia, J.M. and Ruan, Y.  
Genome Institute of Singapore, Zebrafish EST Collection  
Unpublished  
JOURNAL  
TITLE  
COMMENT  
Contact: Ruan Y  
Laboratory of Molecular Biotechnology  
Genome Institute of Singapore  
1 Science Park Road, The Capricorn #05-01, Singapore 117528  
Tel: +65 6827 5200  
Fax: +65 6827 5201  
Email: glary@nus.edu.sg  
GIS Clone ID: ZF001-P00049-PP\_L20  
PCR Primers  
FORWARD: M13  
BACKWARD: M13  
Plate: ZF001-P00049-DPE-F2-D  
Seq primer: CGCATTAAGTGTATAGCA  
High quality sequence stop: 67.  
Location/Qualifiers  
1..67  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:6910149"  
/issue\_type="Embryo"  
/dev\_stage="7 Different embryonic Stages (From just  
fertilized Embryos to 72 hours just hatched baby fish)"  
/lab\_host="DH10B"  
/clone lib="GISZP001"  
/note="Vector: pMR-LIB, site 1: Sfi A (GGCCATTAGCGCC) /  
site 2: Sfi B (GGCCGCTTGGCC) / Priming method: Sfi-(dT)30  
primed; Priming sequence: 5-ATTCTAGA GGCCGAGCGCGCC  
GACATG(T)30VN; Directionally cloned, 5' cloning site:  
Sfi A site GGCCATTAGCGCC; 3' cloning site: Sfi B  
5-AGCAGTGTATACAGCAGAGAGCGCC; 3' linker/adaptor sequence:  
same as the priming sequence; Average insert size: 2kb; For  
PCR insert analysis: Use M13 Forward and reverse primers;  
Library Amplified Recombinants (inserts): 98; Library  
complexity: 5x10<sup>6</sup>; Full-length construction (method):  
SMART, a Clontech method; Library constructed by: S.  
Mathavan, Chia-lin Wei, and Yijun Ruan Genome Institute of  
Singapore"

## BASE COUNT

19 a 19 c 14 g 15 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 14; Length 67;  
 Best Local Similarity 75.0%; Pred. No. 2.4e+04;  
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RGGCTAGGCHACACGA 16  
 |||||:|||||  
 33 GGCTAGCCACACACA 48

RESULT 7  
 T87H090 86 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. brucei sheared genomic DNA clone 87h09, reverse sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL459831 GI:11861863  
 VERSION AL459831  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 REFERENCES 1 (bases 1 to 86)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Kejaandream, M.A. and Barrell, B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, ed. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: neilsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
 Location/Qualifiers

FEATURES  
 source 1..86  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="87h09"

BASE COUNT 23 a 23 c 18 g 22 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 29; Length 86;  
 Best Local Similarity 85.7%; Pred. No. 2.6e+04;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 GCTAGCHACACGA 16  
 |||||:|||||  
 31 GCTAGACACACGA 44

RESULT 8  
 AA953865 88 bp mRNA linear EST 07-MAY-1998  
 LOCUS on76a12.61 Soares NFL\_T GBC\_S1 Homo sapiens cDNA clone  
 DEFINITION IMAGE:1562590 3' similar to TR:Q92615 Q92615 MYELOBLAST KIA0217 ;,  
 mRNA sequence.  
 ACCESSION AA953865  
 VERSION AA953865.1 GI:3116783  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 88)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapdb-remail.nih.gov](mailto:cgapdb-remail.nih.gov)  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Trace considered overall poor quality  
 Seq primer: -40m3 fwd. RT from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

FEATURES  
 source 1..88  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1562590"  
 /lab\_host="DH10B"  
 /clone\_1lb="Soares NFL\_T GBC\_S1"  
 /note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NDHL19W, testis NRT, and B-cell  
 NCI-CGAP GC81) were mixed, and 88 circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 1.M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT 17 a 20 c 34 g 17 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 9; Length 88;  
 Best Local Similarity 85.7%; Pred. No. 2.7e+04;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGCTAGCHACACG 15  
 |||||:|||||  
 61 GGCTGGCCACACG 74

RESULT 9  
 AZ602406 90 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0421H09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0421H09 F, genomic survey sequence.  
 ACCESSION AZ602406  
 VERSION AZ602406.1 GI:11724596  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 90)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0421 row: H column: 09  
 Seq primer: CGTGTAAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 90.  
 Location/Qualifiers

## FEATURES

source

1..90  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U061M0421H09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid U061M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF159072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

14 a 18 c 28 g 30 t

## ORIGIN

Query Match 72.5%; Score 11.6; DB 28; Length 90;  
 Best Local Similarity 75.0%; Pred. No. 2.7e+04;  
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy

1 RGGCTAGCHACACGA 16  
 : |||||: |||||:  
 65 AGGCTGGCCACACACTA 50

Db

RESULT 10  
 BH215494/c  
 LOCUS  
 DEFINITION BH215494 93 bp DNA linear GSS 08-NOV-2001  
 1006027C12.2EL y2 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.  
 ACCESSION BH215494  
 VERSION BH215494.1 GI:16806152  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 93)  
 Walbot, V.  
 Maize genomic sequences found using engineered RescueMu transposon  
 Unpublished  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Reverse complemented post-ligation sequence from source sequence.  
 Plate: 1006027 row: 42  
 Class: transposon-tagged.  
 Location/Qualifiers

## FEATURES

source

1..93  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /clone\_1ib="1006 - RescueMu Grid G"  
 /note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site\_1: BamHI; Site\_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.instate.edu' and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## BASE COUNT

15 a 17 c 39 g 22 t

## ORIGIN

Query Match 72.5%; Score 11.6; DB 28; Length 93;  
 Best Local Similarity 85.7%; Pred. No. 2.7e+04;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy

2 GCGTAGCHACACG 15  
 |||||: |||||:  
 17 GCGAAGCACACACG 4

Db

RESULT 11  
 BG695449/c  
 LOCUS  
 DEFINITION BG695449 99 bp mRNA linear EST 04-MAY-2001  
 NISC IV17E07.w2 Soares NMSP2 pituitary Mus musculus cDNA clone IMAGE:4318212 5', mRNA sequence.  
 ACCESSION BG695449  
 VERSION BG695449.1 GI:13955375  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathli; Muridae; Murinae; Mus.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 cDNA Library Preparation: M. Bento Soares Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium/LLNL  
 Sequencing Center (NISC)  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
 MGI:1598980  
 Plate: LLAM9923 row: K column: 13  
 Seq primer: T7 primer.

## FEATURES

source

1..99  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4318212"  
 /tissue\_type="pituitary gland"

```

/dev stage="embryo, 14 dpc"
/lab host="DH10B (phage-resistant)"
/clone_lib="Soares NMMP2 pituitary"
/note="Organ: Brain; Vector: pT73D-Pac; Site 1: NotI,
Site 2: EcoRI; 1st strand cDNA was primed with a NotI -
oligo(dT) primer
5'-ACTGGAAGATTGGGGCGGGCGCTTTTCTTTTCTTTT-3';
double-stranded cDNA was ligated to EcoRI adaptors
5'-AATTCGCGACGAG-3' AND 5'-CTGTGTCGCG-3' (Pharmacia),
digested with NotI and cloned into the NotI and EcoRI
sites of the pT73D-Pac vector. Library went through one
round of normalization, and was constructed in the
laboratory of M. Bento Soares (University of Iowa)."
```

BASE COUNT 10 a 21 c 33 g 35 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 10; Length 99;  
Best Local Similarity 75.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
|||||:|||||  
76 GGGTTAGCACACACAA 61

Db

RESULT 12  
B0625306 100 bp mRNA linear EST 01-JUL-2002  
LOCUS rd27g03.y1 Meloidogyne incognita egg SL1 TOPO v1 Meloidogyne  
DEFINITION incognita cDNA 5', mRNA sequence.  
B0625306  
VERSION B0625306.1 GI:21652484  
KEYWORDS EST.  
SOURCE Meloidogyne incognita (southern root-knot nematode)  
ORGANISM Meloidogyne incognita  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heterodera; Meloidogyminae; Meloidogyne.  
1 (bases 1 to 100)  
McCartter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wyle,T.,  
Dante,M., Maria,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,  
Gibbons,M., Rifter,S., Bennett,J., Franklin,C., Tsagarisvili,R.,  
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe  
,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,  
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and  
Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished  
Contact: McCartter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: eswatson.wustl.edu  
The library was constructed by Claire Murphy and Dr. James McCartter  
at Washington University, St. Louis. Meloidogyne incognita eggs  
were provided by Andrew Kloek of Divergence Inc., St. Louis, MO.  
Putative full length read  
The vector to vector length is 101  
Seq primer: -40R from Gibco.  
Location/Qualifiers  
1..100  
/oranism="Meloidogyne incognita"  
/mol type="mRNA"  
/db xref="taxon:6306"  
/dev stage="egg"  
/lab host="DH10B (Invitrogen)"  
/clone\_lib="Meloidogyne incognita egg SL1 TOPO v1"  
/note="Vector: pCRIT-TOPO (Invitrogen); Site 1: EcoRI;  
Site 2: EcoRI; The library was constructed by Claire  
Murphy and Dr. James McCartter at Washington University,  
St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR  
products of size >400 nucleotides containing SL1 on the 5'.

```

end and oligo(dT) on the 3' end were non-directionally  

cloned into pCRIT-TOPO(Invitrogen) following the TOPO TA  

cloning protocol. Meloidogyne incognita eggs were provided  

by Andrew Kloek of Divergence Inc., St. Louis, MO."
```

BASE COUNT 39 a 29 c 15 g 17 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 13; Length 100;  
Best Local Similarity 75.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
|||||:|||||  
30 AGCCGACACACACAA 45

Db

RESULT 13  
BH901408 26 bp DNA linear GSS 04-SEP-2002  
LOCUS SALK\_079024.36.15.x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_079024.36.15.x, genomic  
survey sequence.  
BH901408  
ACCESSION BH901408.1 GI:22712289  
VERSION BH901408  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosid II; Brassicales; Brassicaceae; Arabidopsie.  
1 (bases 1 to 26)  
Alonso,J.M., Leisner,J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.  
A sequence-indexed library of insertion Mutations in the  
Arabidopsis Genome  
Unpublished  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1..26  
/oranism="Arabidopsis thaliana"  
/mol type="genomic DNA"  
/strain="Columbia 0"  
/db xref="taxon:3702"  
/clone="SALK\_079024.36.15.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

```

FEATURES  

source  

1..26  

/oranism="Arabidopsis thaliana"  

/mol type="genomic DNA"  

/strain="Columbia 0"  

/db xref="taxon:3702"  

/clone="SALK_079024.36.15.x"  

/clone_lib="Arabidopsis thaliana TDNA insertion lines"  

/note="PCR was performed on Arabidopsis thaliana lines  

each of which contains one or more TDNA insertion  

elements. The resultant fragment for each line was  

directly sequenced to determine the genomic sequence at  

the site of insertion. Details of the protocols used can  

be found at http://signal.salk.edu/cdna\_protocols.html"
```

BASE COUNT 6 a 6 c 3 g 11 t

ORIGIN

Query Match 70.0%; Score 11.2; DB 28; Length 26;  
Best Local Similarity 91.7%; Pred. No. 2.8e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGGTACGACACAA 13  
|||||:|||||  
21 GGGTACGACACAA 10

Db

RESULT 14  
 A0025306/c 34 bp DNA linear GSS 23-AUG-2000  
 LOCUS EP(3)313 Drosophila melanogaster EP line Drosophila melanogaster  
 DEFINITION genomic Sequence recovered from 5' end of P element, genomic survey  
 sequence.  
 ACCESSION A0025306  
 VERSION A0025306.1 GI:3265658  
 KEYWORDS GSS.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 34)  
 Liao,G.-C., Rehm,E.J. and Rubin,G.M.  
 Insertion site preferences of the P transposable element in  
 Drosophila melanogaster  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)  
 JOURNAL 20202638  
 MEDLINE 10716700  
 PUBMED  
 COMMENT Contact: Gerald Rubin  
 Berkeley Drosophila Genome Project  
 University of California, Berkeley  
 USA Building, Berkeley, CA 94720-3200, USA  
 Fax: 5106439947  
 Email: gerry@fruitfly.berkeley.edu  
 Sequence recovery method was inverse PCR.  
 Sequence orientation is forward strand relative to 5' end of P  
 element  
 The P element insertion position is base 27 in the 34 bases. This  
 insertion position refers to the first base of the 8 base target  
 recognition sequence.  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..34  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone\_lib="Drosophila melanogaster EP line"  
 /note="Inverse PCR was performed on Drosophila  
 melanogaster strains each of which contains a single EP  
 transposable element insertion. (The generation of these  
 insertion strains is described in Rorth P, Szabo K, Bailey  
 A, Laverly T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes  
 V, Ansoerge W, Cohen SM. 1998. Systematic gain-of-function  
 genetics in Drosophila. Development 6:1049-1057.) The  
 resultant fragment for each strain was directly sequenced  
 to determine the genomic sequence at the site of  
 insertion. Details of the protocols used can be found at  
 http://fruitfly.berkeley.edu/P\_distrupt/inverse\_pcr.html."

BASE COUNT  
 ORIGIN  
 4 a 13 c 10 g 7 t

Query Match 70.0%; Score 11.2; DB 28; Length 34;  
 Best Local Similarity 78.6%; Pred. No. 3.1e+04;  
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAC 14  
 :|||||:  
 Db 28 AGGCTGCGACAC 15

RESULT 15  
 BH861777/c 49 bp DNA linear GSS 05-AUG-2002  
 LOCUS BH861777  
 DEFINITION SALK\_087974 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
 thaliana genomic clone SALK\_087974, genomic survey sequence.  
 ACCESSION BH861777  
 VERSION BH861777.1 GI:22097103  
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 1 (bases 1 to 49)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
 Zimmerman,J. and Ecker,J.R.  
 A sequence-indexed library of insertion mutations in the  
 Arabidopsis Genome  
 Unpublished  
 JOURNAL Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA. This sequence lies within an annotated exon of At5g01330.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..49  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone\_lib="SALK\_087974"  
 /note="lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at http://signal.salk.edu/tdna\_protocols.html"

BASE COUNT  
 ORIGIN  
 7 a 9 c 15 g 18 t

Query Match 70.0%; Score 11.2; DB 28; Length 49;  
 Best Local Similarity 91.7%; Pred. No. 3.6e+04;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAGCHACACGA 16  
 :|||||:  
 Db 12 TAGCCACACGA 1

RESULT 16  
 BH861778/c 49 bp DNA linear GSS 05-AUG-2002  
 LOCUS BH861778  
 DEFINITION SALK\_087975 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
 thaliana genomic clone SALK\_087975, genomic survey sequence.  
 ACCESSION BH861778  
 VERSION BH861778.1 GI:22097104  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 1 (bases 1 to 49)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
 Zimmerman,J. and Ecker,J.R.  
 A sequence-indexed library of insertion mutations in the  
 Arabidopsis Genome  
 Unpublished  
 JOURNAL Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752

Fax: 858 558 6379  
Email: ecker@sal.k.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated exon of At5g01330.  
Class: TDNA tagged.

# FEATURES

source

1. .49  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK 087975"  
/note="lib-Arabidopsis thaliana TDNA insertion lines"  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

BASE COUNT  
ORIGIN  
7 a 9 c 15 g 18 t

Query Match  
Best Local Similarity 91.7%; Pred. No. 3.6e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAGCCACACGA 16  
Db 12 TAGCCACACGA 1

RESULT 17  
AA142563 55 bp mRNA linear EST 18-FEB-1997  
LOCUS m59b11.r1 Soares thymus 2NdbMT Mus musculus CDNA clone IMAGE:583005  
DEFINITION 5' similar to TR.G1203965 G1203965 BONE-DERIVED GROWTH FACTOR ;,  
mRNA sequence.

ACCESSION AA142563  
VERSION AA142563.1 GI:1711818  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 55)  
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE The Washu-HHMI Mouse EST Project  
JOURNAL Unpublished  
COMMENT Contact: Marra M/Mouse EST Project  
Washu-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LML; contact the  
IMAGE Consortium ([info@image.lml.gov](mailto:info@image.lml.gov)) for further information.  
MG1:357653

# FEATURES

source

1. .55  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:583005"

/sex="male"  
/issue\_type="Thymus"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares thymus 2NdbMT"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand CDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCGAAGGAGGAGCGCGCGCTTTTCTTTTCTTTTCTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through two  
rounds of normalization, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN  
12 a 17 c 13 g 13 t

Query Match  
Best Local Similarity 78.6%; Pred. No. 3.7e+04;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCACAAC 14  
Db 24 GGACTAGCACAAC 37

RESULT 18  
BUB66082 75 bp mRNA linear EST 16-OCT-2002  
LOCUS S062E01 Populus imbed seed CDNA library Populus tremula x Populus  
DEFINITION tremuloides CDNA 5 prime, mRNA sequence:  
ACCESSION BUB66082  
VERSION BUB66082.1 GI:24056736  
KEYWORDS EST.  
SOURCE Populus tremula x Populus tremuloides  
ORGANISM Populus tremula x Populus tremuloides

REFERENCE 1 (bases 1 to 75)  
AUTHORS Uneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.  
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags  
from multiple libraries  
JOURNAL Unpublished  
COMMENT Contact: BHALERAO RUPALI R.  
Umea Plant Science Center  
Department of Plant Physiology  
University of Umea, 901 87 Umea, Sweden  
Tel: +46 90 786 5279  
Fax: +46 90 786 6676  
Email: rupali.bhalerao@plantphys.umu.se.

# FEATURES

source

1. .75  
/organism="Populus tremula x Populus tremuloides"  
/mol\_type="mRNA"  
/db\_xref="taxon:47664"  
/issue\_type="imbed seed"  
/clone\_lib="Populus imbed seed CDNA library"

BASE COUNT  
ORIGIN  
23 a 20 c 12 g 20 t

Query Match  
Best Local Similarity 70.0%; Score 11.2; DB 13; Length 75;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCACAAC 14  
Db 54 AGGCTAGCACAAC 41

RESULT 19  
CA819431

LOCUS CA819431 77 bp mRNA linear EST 09-DEC-2002  
 DEFINITION sau78d01.y1 Gm-cl071 Glycine max cDNA clone SOYBEAN CLONE ID:  
 ACCESSION Gm-cl071-7058 5', mRNA sequence.  
 CA819431  
 VERSION CA819431.1 GI:26268368  
 KEYWORDS EST  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; euroside 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 REFERENCE 1 (bases 1 to 77)  
 AUTHORS Shoemaker, R., Kaim, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna  
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers  
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk  
 R., Rutter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann  
 R., Waterston, R. and Wilson, R.  
 TITLE Public Soybean EST Project  
 JOURNAL Unpublished  
 COMMENT Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: Reggen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntville, AL 35801 For further information  
 call: (800)-533-4363 or contact: cdu@reggen.com web site:  
 www.reggen.com  
 Putative full length read  
 vector to vector length is 78  
 Seq primer: -40RP from Gibco.  
 Location/Qualifiers  
 1..77  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl071-7058"  
 /tissue\_type="immature pods (~2cm long) of greenhouse  
 grown plants"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl071"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; The  
 cDNA library was constructed from mRNA isolated from  
 immature pods (approximately 2cm long) of greenhouse grown  
 plants. The library was prepared using the Life  
 Technologies superscript cDNA library construction kit.  
 Complementary DNA was synthesized from mRNA using a  
 poly(dT) sequence with a NotI restriction site. SalI  
 linkers adapters were ligated to the blunt-ended cDNA  
 fragments followed by NotI digestion. The cDNA fragments  
 were directionally cloned into the NotI-SalI restriction  
 site of the pSPORT1 vector. The ligated cDNA fragments  
 were transformed into E.coli ElectroMax DH10B host cells.  
 This library was constructed in the laboratory of Dr. Lila  
 Vodkin by Anu Khanna at the University of Illinois at  
 Urbana-Champaign. email: l-vodkin@uiuc.edu"

BASE COUNT 18 a 14 c 17 g 28 t  
 ORIGIN  
 Query Match 70.0%; Score 11.2; DB 14; Length 77;  
 Best Local Similarity 91.7%; Pred. No. 4.3e+04;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTAGCAGACAG 15  
 |||||:  
 Db 65 CTAGCCACAG 76  
 RESULT 20

LOCUS AA183068 85 bp mRNA linear EST 07-JAN-1997  
 DEFINITION m86e09.r1 Soares mouse lymph node NbM1N Mus musculus cDNA clone  
 IMAGE:636808 5' similar to TR:G1203965 G1203965 BONE-DERIVED GROWTH  
 FACTOR /, mRNA sequence.  
 ACCESSION AA183068  
 VERSION AA183068.1 GI:1766724  
 KEYWORDS EST  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 85)  
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouse@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:368800  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..85  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:636808"  
 /sex="male"  
 /tissue\_type="lymph node"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares mouse lymph node NbM1N"  
 /note="Organ: lymph node; Vector: pVT73D-Pac (Pharmacia)  
 with a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 15'  
 TGTACCAATCTGAAGTGGGCGCGGAGTACTTTTTTTTTTTTTTTTTTTTTT  
 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pVT73 vector. RNA  
 provided by Dr. Bertrand Jordan. Library constructed and  
 normalized by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 19 a 26 c 21 g 19 t  
 ORIGIN  
 Query Match 70.0%; Score 11.2; DB 9; Length 85;  
 Best Local Similarity 78.6%; Pred. No. 4.4e+04;  
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAC 14  
 :|||:  
 Db 54 GGACTAGCCACAC 67  
 RESULT 21  
 AZ362937 92 bp DNA linear GSS 02-OCT-2000  
 LOCUS 1M0108B18F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0108B18 F, genomic survey sequence.

ACCESSION AZ362937  
 VERSION AZ362937.1 GI:10476637  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 92)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weis  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0108 row: B column: 18  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 92.  
 FEATURES  
 source  
 1..92  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0108B18"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gbl/AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Arabidopsis thaliana genomic clone SALK\_120055.25.10.x, genomic survey sequence.  
 ACCESSION BZ291268  
 VERSION BZ291268.1 GI:24336251  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 REFERENCE 1 (bases 1 to 92)  
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.  
 TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
 JOURNAL Unpublished  
 COMMENT Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g17970. Class: TDNA tagged.  
 FEATURES  
 source  
 1..92  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_120055.25.10.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

BASE COUNT 21 a 25 c 30 g 16 t  
 ORIGIN  
 Query Match 70.0%; Score 11.2; DB 28; Length 92;  
 Best Local Similarity 78.6%; Pred. No. 4.6e+04;  
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 23  
 LOCUS BZ291268/c 95 bp mRNA linear EST 16-OCT-2002  
 DEFINITION S075A07 Populus imbricad seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.  
 ACCESSION BZ291268  
 VERSION BZ291268.1 GI:24057814  
 KEYWORDS EST.  
 SOURCE Populus tremula x Populus tremuloides  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 REFERENCE 1 (bases 1 to 95)  
 AUTHORS Umeberg, P., Bhalerao, R.R., Jansson, S., and Sterky, F.  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 JOURNAL Unpublished  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center

Department of Plant Physiology  
University of Umea, 901 87 Umea, Sweden  
Tel: +46 90 786 5279  
Fax: +46 90 786 6678  
Email: rupall.bhalerao@plantphys.umu.se.  
Location/Qualifiers

## FEATURES

source

1.95  
/organism="Populus tremula x Populus tremuloides"  
/mol\_type="mRNA"  
/db\_xref="taxon:47664"  
/tissue\_type="imbibed seed"  
/clone\_lib="Populus imbibed seed cDNA library"

## BASE COUNT

25 a 28 c 16 g 26 t

## ORIGIN

Query Match 70.0%; Score 11.2; DB 13; Length 95;  
Best Local Similarity 78.6%; Pred. No. 4.6e+04;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAC 14  
:|||||||:  
74 AGGCTAGCTAGAAC 61

## RESULT 24

BU862306 96 bp mRNA linear EST 16-OCT-2002  
LOCUS BU862306/c  
DEFINITION Sol14A04 Populus imbibed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION BU862306 GI:24048366  
VERSION BU862306  
KEYWORDS EST.  
SOURCE Populus tremula x Populus tremuloides  
ORGANISM Populus tremula x Populus tremuloides  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eucosids I; Malpighiales; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 96)  
Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
The poplar tree transcriptome: Analysis of expressed sequence tags  
from multiple libraries

JOURNAL Unpublished  
CONTACT: BHALERAO RUPALI R.  
Umea Plant Science Center  
Department of Plant Physiology  
University of Umea, 901 87 Umea, Sweden  
Tel: +46 90 786 5279  
Fax: +46 90 786 6678  
Email: rupall.bhalerao@plantphys.umu.se.

## FEATURES

source

1.96  
/organism="Populus tremula x Populus tremuloides"  
/mol\_type="mRNA"  
/db\_xref="taxon:47664"  
/tissue\_type="imbibed seed"  
/clone\_lib="Populus imbibed seed cDNA library"

## BASE COUNT

27 a 27 c 16 g 26 t

## ORIGIN

Query Match 70.0%; Score 11.2; DB 13; Length 96;  
Best Local Similarity 78.6%; Pred. No. 4.6e+04;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAC 14  
:|||||||:  
46 AGGCTAGCTAGAAC 33

## RESULT 25

AW797834 100 bp mRNA linear EST 16-MAY-2000  
LOCUS AW797834/c  
DEFINITION CMO-UM0042-020300-261-e05 UM0042 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW797834

VERSION AW797834.1 GI:7849704  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS

1 (bases 1 to 100)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsushima, A., Baita, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (??), 3491-3496 (2000)  
MEDLINE 20202663  
PubMed 10737800

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=CMO-UM0042-020  
300-261-e05&cl3=2000-03-02&cl4=1)

Seq primer: puc 18 forward  
High quality sequence start: 8  
High quality sequence stop: 100.  
Location/Qualifiers

## FEATURES

source

1.100  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/def\_strage="Adult"  
/clone\_lib="UM0042"  
/note="Organ: uterus; Vector: puc18; Site\_1: Sma1; Site\_2:  
Sma1; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

## BASE COUNT

16 a 34 c 26 g 24 t

## ORIGIN

Query Match 70.0%; Score 11.2; DB 9; Length 100;  
Best Local Similarity 91.7%; Pred. No. 4.7e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAGCCACACCA 16  
:|||||||:  
Db 15 TAGCCACACCA 4

## RESULT 26

BM328423 100 bp mRNA linear EST 04-JAN-2002  
LOCUS BM328423/c  
DEFINITION PIC1\_29\_B03\_g1\_A002 Pathogen-infected compatible 1 (PIC1) Sorghum  
bicolor cDNA, mRNA sequence.

ACCESSION BM328423 GI:18067560  
VERSION BM328423  
KEYWORDS EST.  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD  
clade; Panicoideae; Andropogoneae; Sorghum.

## REFERENCE

1 (bases 1 to 100)

**AUTHORS** Cordonnier-Pratt, M.-M., Gingle, A., Pang, G.C., Dean, R., Wing, R., Sudman, M. and Pratt, L.H.  
**TITLE** An EST database from Sorghum: plants infected with a compatible pathogen  
**JOURNAL** Unpublished  
**COMMENT** Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmp@uga.edu  
 Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTrak or 17 sequencing primer, are presented as the reverse complement.  
 Seq primer: 77  
 High quality sequence start: 30  
 High quality sequence stop: 100  
 PolyA=yes

**FEATURES**  
 source  
 1..100  
 /organism="Sorghum bicolor"  
 /mol\_type="mRNA"  
 /cultivar="BTx623"  
 /db\_xref="taxon:4558"  
 /tissue\_type="leaves"  
 /dev\_stage="4-week-old seedlings infected with Colletotrichum graminicola"  
 /clone\_lib="Pathogen-infected compatible 1 (PIC1)"  
 /note="Vector: pInscript II SK(-) from lambda Zap II; Site 1: XhoI; Site 2: EcoRI. Four-week-old sorghum seedlings were sprayed with spore suspension prepared from 3-week-old RM421, a sorghum isolate of the anthracnose pathogen Colletotrichum graminicola. Inoculated plants were kept in a 25 C dark growth chamber with 100% relative humidity for 24 hr, followed by 12/12 hr of light/dark cycle at 25 C with 90% relative humidity for another 24 hr. All leaves were harvested and quick frozen with liquid nitrogen and stored in a -80 C freezer. The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision.  
 WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."  
 BASE COUNT 30 a 15 c 24 g 31 t  
 ORIGIN

Query Match 70.0%; Score 11.2; DB 12; Length 100;  
 Best Local Similarity 91.7%; Pred. No. 4.7e+04;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**Qy** 4 CTAGCACAACG 15  
 |||||  
 26 CTAGCACAACG 15

**Db** 26 CTAGCACAACG 15

**RESULT 27**  
 BUB61867 100 bp mRNA linear EST 16-OCT-2002  
 BUB61867/c  
 LOCUS S007G10 Populus imbed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.  
 ACCESSION BUB61867  
 VERSION BUB61867.1 GI:24047927  
 KEYWORDS EST.  
 SOURCE Populus tremula x Populus tremuloides  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Malpighiales; Salicaceae; Populus.  
 REFERENCE 1 (bases 1 to 100)  
 UNEBERG, P., BHALERIO, R.R., JANSSEN, S. and STECKY, F.  
 The poplar tree transcriptome: Analysis of expressed sequence tags

**JOURNAL** from multiple libraries  
**COMMENT** Unpublished  
 Contact: BHALERIO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalero@plantphys.umu.se

**FEATURES**  
 source  
 1..100  
 /organism="Populus tremula x Populus tremuloides"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:47664"  
 /tissue\_type="imbibed seed"  
 /clone\_lib="Populus imbed seed cDNA library"  
 BASE COUNT 22 a 29 c 20 g 29 t  
 ORIGIN

Query Match 70.0%; Score 11.2; DB 13; Length 100;  
 Best Local Similarity 78.6%; Pred. No. 4.7e+04;  
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 RGCTAGCACAAC 14  
 :|||  
 37 AGCTAGCTAGAC 24

**Db** 37 AGCTAGCTAGAC 24

**RESULT 28**  
 CC179318 74 bp DNA linear GSS 02-MAY-2003  
 LOCUS SALK\_067813.35.30.x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_067813.35.30.x, genomic survey sequence.  
 ACCESSION CC179318  
 VERSION CC179318.1 GI:30317869  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 74)  
 ALONSO, J.M., LEISE, T.J., BARAJAS, P., CHEN, H., CHEUK, R., GADRINAB, C., JESKE, A., KARNES, M., KIM, C.J., PARKER, H., PEDRINS, L., SHIM, P., ZIMMERMAN, J. and ECKER, J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
 Unpublished  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: eckere@salk.edu  
 This is single pass sequence recovered from the left border of TDNA.  
 Class: TDNA tagged.  
**FEATURES**  
 source  
 1..74  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 27 a 9 c 13 g 25 t  
 ORIGIN

Query Match 68.8%; Score 11; DB 29; Length 74;  
 Best Local Similarity 80.0%; Pred. No. 5.4e+04;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCTAGCACAACA 16  
 |||||  
 64 GGCTGCAACATGA 50

Db

RESULT 29  
 U44372 79 bp mRNA linear EST 03-APR-1996  
 U44372/c  
 LOCUS  
 DEFINITION EN04372 Aspergillus nidulans cleistothecium Emericella nidulans  
 CDNA clone SE0877, mRNA sequence.  
 ACCESSION U44372  
 VERSION U44372.1 GI:1245035  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Emericella nidulans (anamorph: Aspergillus nidulans)  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; Emericella.  
 1 (bases 1 to 79)  
 Lee, D., Lee, S., Hwang, H., Kim, J. and Chae, K.  
 Quantitative analysis of gene expression in sexual structures of  
 Aspergillus nidulans by sequencing of 3'-directed CDNA clones  
 FEMS Microbiol. Lett. 138 (1), 71-76 (1996)  
 96236220  
 8674973  
 COMMENT Contact: Keon-Sang Chae  
 Chonbuk National University  
 Chonju, 561-756, S. Korea  
 Tel: +82-652-70-3340  
 Fax: +82-652-70-3345  
 Email: chaeks@chonbukns.chonbuk.ac.kr.  
 Location/Qualifiers  
 FEATURES  
 source  
 1. 79  
 /organism="Emericella nidulans"  
 /mol\_type="mRNA"  
 /strain="FGSC4"  
 /db\_xref="taxon:162425"  
 /clone="SE0877"  
 /issue\_type="cleistothecium"  
 /cell\_type="hull cell"  
 /dev\_stage="sexual"  
 /clone\_id="Aspergillus nidulans cleistothecium"  
 /note="3'-directed CDNA clones; single-pass sequencing"

BASE COUNT 24 a 9 c 20 g 26 t  
 ORIGIN

Query Match 68.8%; Score 11; DB 14; Length 79;  
 Best Local Similarity 80.0%; Pred. No. 5.6e+04;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCTAGCACAACA 16  
 |||||  
 49 GACTGACCAACAAGA 35

Db

RESULT 30  
 AA594999 82 bp mRNA linear EST 26-SEP-1997  
 AA594999  
 LOCUS  
 DEFINITION ns01806.81 NCI CGAP Pr22 Homo sapiens CDNA clone IMAGE:1102306 3'  
 similar to TR:G1234841 G1234841 LIM PROTEIN MLP.; mRNA sequence.  
 ACCESSION AA594999  
 VERSION AA594999.1 GI:2410349  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 82)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Email: cgaps-remail.nih.gov  
 Contact: Robert Straubeberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 www-bio.livn.gov/bdip/image/image.html

Trace considered overall poor quality  
 Insert Length: 968 Std Error: 0.00  
 Seg primer: -40ml3 fwd. RT from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 82  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1102306"  
 /sex="male"  
 /issue\_type="normal prostate"  
 /lab\_host="DH10B"  
 /clone\_id="NCI-CGAP Pr22"  
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)  
 with a modified polylinker; 1st strand cDNA was prepared  
 from normal prostate bulk tissue, and was then primed with  
 a Not I - o150(4R) primer. Double-stranded cDNA was  
 ligated to Eco RI adaptors (Pharmacia), digested with Not  
 I and cloned into the Not I and Eco RI sites of the  
 modified pT73 vector. Library is normalized, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 23 a 25 c 21 g 13 t  
 ORIGIN

Query Match 68.8%; Score 11; DB 9; Length 82;  
 Best Local Similarity 80.0%; Pred. No. 5.7e+04;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCTAGCACAACA 16  
 |||||  
 63 GACTTGCCACAACA 77

Db

RESULT 31  
 BE330980 100 bp mRNA linear EST 04-DEC-2001  
 BE330980  
 LOCUS  
 DEFINITION s092a05.y1 Gm-c1041 Glycine max CDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-c1041-777 5', similar to TR:Q42897 Q42897 UBIQUITIN-CONUGATING  
 ENZYME E2.; mRNA sequence.  
 ACCESSION BE330980  
 VERSION BE330980.1 GI:9204756  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Glycine max (soybean)  
 Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 100)  
 Shoemaker, R., Keim, P., Vodkin, L., Expelling, J., Coryell, V., Khanna  
 A., Bolla, B., Merris, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers  
 R., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk  
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann  
 R., Waterston, R. and Willson, R.  
 Public Soybean EST Project

JOURNAL  
COMMENT

Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Trace considered overall poor quality This clone is available  
through: Resgen, Invitrogen Corp, 2130 South Memorial Parkway  
Huntsville, AL 35801 For further information call: (800)-533-4363  
or contact via email: ccu@resgen.com  
High quality sequence stop: 1.

## FEATURES

## source

Location/Qualifiers  
1. .100  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl041-777"  
/tissue\_type="Senescing leaves, mature plant, greenhouse  
grown"  
/lab\_host="DH10B"  
/clone\_id="Gm-cl041"  
/note="Vector: pRT3Pac (Pharmacia); Site 1: EcoRI,  
Site 2: HindIII; This library was constructed from mRNA  
isolated from senescing leaf tissue of mature greenhouse  
grown plants of the cultivar Williams. Complementary DNA  
was synthesized from mRNA using a 3' anchored poly(dT)  
primer. EcoRI adapters were ligated to the blunt-ended  
cDNA fragments followed by digestion with EcoRI and  
HindIII. The cDNA fragments were directionally cloned  
into the EcoRI-HindIII restriction site of the pRT3-Pac  
vector. The ligated cDNA fragments were transformed into  
DH10B host cells. This library was constructed by Dr.  
Randy Shoemaker."

BASE COUNT  
ORIGIN

29 a 25 c 27 g 19 t

Query Match 68.8%; Score 11; DB 10; Length 100;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGCTAGGCAACGA 16  
Db 78 GGCAAGCAACATCA 92

## RESULT 32

## LOCUS

AU106358 50 bp mRNA linear EST 30-AUG-2001  
AU106358 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HEP02980, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tanoda, T., Mizushima-Sugano, J., Sese, J., Hara  
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
, S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1. .50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HEP02980"  
/clone\_id="Sugano Homo sapiens cDNA library"

## FEATURES

## source

BASE COUNT  
ORIGIN

3 a. 20 c 12 g 15 t

Query Match 67.5%; Score 10.8; DB 9; Length 50;  
Best Local Similarity 85.7%; Pred. No. 6.1e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GGCTAGGCAACGA 16  
Db 31 GGCAAGCAACATCA 18

## RESULT 33

## LOCUS

BZ287687 72 bp DNA linear GSS 24-OCT-2002  
BZ287687  
SALK\_021065.27.75.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_021065.27.75.x, genomic  
survey sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

BZ287687  
SALK\_021065.27.75.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_021065.27.75.x, genomic  
survey sequence.  
BZ287687  
BZ287687.1 GI:24325988  
GSS.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
1 (bases 1 to 72)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgil, N.  
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,  
, Zimmerman, J. and Ecker, J.R.  
A sequence-indexed library of insertion mutations in the  
Arabidopsis Genome  
Unpublished  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1. .72  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_id="SALK\_021065.27.75.x"  
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/cdna\\_protocol.html](http://signal.salk.edu/cdna_protocol.html)

## FEATURES

## source

BASE COUNT  
ORIGIN

22 a 12 c 14 g 24 t

Query Match 67.5%; Score 10.8; DB 29; Length 72;  
Best Local Similarity 85.7%; Pred. No. 7e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCTAGCAGACCA 16  
 Db 52 GCTAGCAGACCAATGA 65

RESULT 34  
 LOCUS AZ619815/c 80 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0452018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0452018 F, genomic survey sequence.

ACCESSION AZ619815  
 VERSION AZ619815.1 GI:11742005  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 80)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.  
 and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0452 row: D column: 18  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 80.  
 Location/Qualifiers

FEATURES  
 SOURCE 1..80  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0452018"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 20 a 15 c 21 g 24 t  
 ORIGIN  
 Query Match 67.5%; Score 10.8; DB 28; Length 80;  
 Best Local Similarity 83.3%; Pred. No. 7.3e+04;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGCTAGCHACA 12  
 Db 28 AGGCTAGCTACA 17

RESULT 35  
 LOCUS AL947273 85 bp DNA linear GSS 24-OCT-2002  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-303A09-015560,  
 genomic survey sequence.

ACCESSION AL947273  
 VERSION AL947273.1 GI:24403895  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.  
 and Weishaar, B.  
 A pipeline for automated high-throughput generation of FSTs  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines

TITLE Unpublished  
 JOURNAL  
 COMMENT Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.  
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 for flanking sequence tag based reverse genetics  
 Unpublished  
 3 (bases 1 to 85)  
 Li, Y., Strizhov, N., Rosso, M. and Weishaar, B.  
 Direct Submission  
 Submitted (21-OCT-2002) Weishaar B., Max-Planck-Institut fuer  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence is recovered from the left border of the T-DNA. It  
 indicates an insertion close to or within gene At3g25560. The  
 sequences are generated at the MPI for Plant Breeding Research in  
 the context of the GABI-Kat project. GABI-Kat is part of the German  
 Plant Genomics program designated 'GABI'. Information on line  
 availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES  
 SOURCE 1..85  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-303A09-015560"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector PAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

BASE COUNT 27 a 19 c 18 g 21 t  
 ORIGIN  
 Query Match 67.5%; Score 10.8; DB 29; Length 85;  
 Best Local Similarity 83.3%; Pred. No. 7.5e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGCTAGCHACA 12  
 Db 26 AGGCTAGCACA 37

RESULT 36  
W17739 92 bp mRNA linear EST 10-SEP-1996  
LOCUS m57792.r1 Soares mouse p3NMP19.5 Mus musculus cDNA clone  
DEFINITION IMAGE:335474 5', mRNA sequence.  
W17739  
ACCESSION W17739.1 GI:1292123  
VERSION EST.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:216874  
Seq primer: mob.REGA+RT  
High quality sequence stop: 85.  
Location/Qualifiers  
1. .92  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:335474"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares mouse p3NMP19.5"  
/note="Vector: pRT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCCGCAATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."  
BASE COUNT 30 a 25 c 25 g 12 t  
ORIGIN  
Query Match 67.5%; Score 10.8; DB 14; Length 92;  
Best Local Similarity 83.3%; Pred. No. 7.7e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 RGGCTAGCACA 12  
Db 74 GGGCTAGCACA 85

RESULT 37  
BZ291056 94 bp DNA linear GSS 24-OCT-2002  
LOCUS SALK\_112368.45.85.x Arabidopsis thaliana TNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_112368.45.85.x, genomic survey sequence.  
ACCESSION BZ291056  
VERSION BZ291056.1 GI:24335637  
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
REFERENCE  
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shum, P., Zimmerman, J., and Ecker, J.R.  
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
JOURNAL Unpublished  
COMMENT Contact: Joseph R. Ecker  
The Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atsg04660. Class: TDNA tagged.  
Location/Qualifiers  
1. .94  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_112368.45.85.x"  
/note="SALK\_112368.45.85.x" cDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"  
BASE COUNT 18 a 24 c 19 g 33 t  
ORIGIN  
Query Match 67.5%; Score 10.8; DB 29; Length 94;  
Best Local Similarity 85.7%; Pred. No. 7.8e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 3 GCTAGCACAACA 16  
Db 35 GCTAGCACAACA 22

RESULT 38  
AA919502 95 bp mRNA linear EST 20-APR-1998  
LOCUS v220g11.r1 Stragene mouse heart (#937316) Mus musculus cDNA clone  
DEFINITION IMAGE:1316324 5', similar to TR:Q60961 Q60961 MEMBRANE TRANSPORTER PROTEIN; mRNA sequence.  
AA919502  
ACCESSION AA919502.1 GI:3066281  
VERSION EST.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseset@atlas.com.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lln.gov) for further information.  
 MGI:686620  
 Seq primer: -28m3 rev1 ET from Amersham  
 High quality sequence stop: 70.  
 Location/Qualifiers

## FEATURES

source

```

1..95
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1316324"
/sex="pooled"
/issue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GATTCGGCAGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

```

## BASE COUNT

20 a 24 c 33 g 18 t

## ORIGIN

Query Match 67.5%; Score 10.8; DB 9; Length 95;  
 Best Local Similarity 75.0%; Pred. No. 7.8e+04;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 RGCTAGCHACACGA 16  
 :|||||  
 Db 32 CGGCTGGCAGACGA 47

## RESULT 39

AZ639727 32 bp DNA linear GSS 14-DEC-2000  
 LOCUS 10501D21F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 DEFINITION clone UGCGM0501D21 F, genomic survey sequence.

ACCESSION AZ639727.1 GI:11763127

## VERSION

AZ639727.1 GI:11763127

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

## REFERENCE

1 (bases 1 to 32)

## AUTHORS

Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.,  
 and Wright, D., Weis, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## JOURNAL

Unpublished

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0501 row: D column: 21  
 Seq primer: CGTGTAAACGACGCGCACT  
 Class: plasmid ends  
 High quality sequence stop: 32.  
 Location/Qualifiers

## FEATURES

1..32

## BASE COUNT

11 a 9 c 3 g 9 t

## ORIGIN

Query Match 66.2%; Score 10.6; DB 28; Length 32;  
 Best Local Similarity 84.6%; Pred. No. 6.6e+04;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 4 CTAGCHACACGA 16  
 :|||||  
 Db 1 CTAGCCCAACTA 13

## RESULT 40

CB305210 37 bp mRNA linear EST 01-JUN-2003  
 LOCUS 3EST-NF1y-025 Drosophila melanogaster cDNA library Drosophila  
 DEFINITION melanogaster cDNA 3', mRNA sequence.

ACCESSION CB305210.1 GI:31297614

## VERSION

CB305210.1 GI:31297614

## KEYWORDS

EST.

## SOURCE

Drosophila melanogaster (fruit fly)

## ORGANISM

Drosophila melanogaster

## REFERENCE

1 (bases 1 to 37)

## AUTHORS

Lee, S., Zhou, G., Bao, J., Shapiro, J., Xu, J., Sun, M., Lin, W., Zhang,  
 R., Chen, J., Clark, T., Sun, M., Wang, J., Johnson, D., Tseng, C., Yang,  
 H., Wang, J., Du, W., Wu, C. I., Zhang, X. and Wang, S. M.

## TITLE

Novel SAGE tags represent a significant number of novel genes in  
 Drosophila genome

## JOURNAL

Unpublished

## COMMENT

Contact: Wang SM

## JOURNAL

Hem/Onc

## COMMENT

University of Chicago Medical Center  
 5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA  
 Tel: 773-702-6788  
 Fax: 773-702-3002  
 Email: swangl@midway.uchicago.edu

This EST was detected from Drosophila melanogaster cDNA library  
 with GluI technique (Generation of longer cDNA fragments from SAGE  
 tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349,  
 2000). A high-throughput GluI procedure for converting a large  
 number of SAGE tag sequences into 3' ESTs. Genes, Chromosomes &  
 Cancers 33:252-261, 2002), which covers from the 3' end of cDNA  
 till the first CATTG.

Seq primer: M13 Forward.  
FEATURES  
Location/Qualifiers  
source  
1..37  
/organism="Drosophila melanogaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/clone\_lib="Drosophila melanogaster cDNA Library"  
BASE COUNT  
7 a 9 g 8 g 13 c  
ORIGIN  
Query Match 66.2%; Score 10.6; DB 14; Length 37;  
Best Local Similarity 84.6%; Pred. No. 7e+04;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 CTAGCHACACGA 16  
|||:|||||  
Db 12 CTAGCCACGACGA 24

Search completed: January 21, 2004, 08:16:38  
Job time : 1412 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 05:18:03 ; Search time 151.5 Seconds  
(without alignments)  
285.089 Million cell updates/sec

Title: US-09-423-035B-122

Perfect score: 16  
Sequence: 1 rgcgtagchacaagca 16

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2722628

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : N\_Geneseq 19Jun03:\*

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24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*  
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	92.5	16	20	AAV82954
2	14.8	92.5	16	20	AAV82953
3	14.8	92.5	16	21	AAV63474
4	14.8	92.5	16	21	AAV63475
5	14.8	92.5	16	22	AAV02749
6	14.8	92.5	16	22	AAV97756
7	14.8	92.5	16	23	ABK09278
8	14.8	92.5	16	24	ABK61076

9	14.8	92.5	16	24	ABK22719	DNAzyme motif. Sy
10	14.8	92.5	16	25	ACA10109	Necrosis factor ka
11	14.8	92.5	16	25	ABZ58432	DNAzyme motif. Sy
12	14.8	92.5	17	25	ABZ66525	Human HER2 synthe
13	14.8	92.5	27	25	ABZ66527	Human HER2 synthe
14	14.8	92.5	29	20	AAZ24361	Nucleic acid-based
15	14.8	92.5	29	20	AAZ24363	Nucleic acid-based
16	14.8	92.5	29	21	AAZ24363	Hammerhead ribozym
17	14.8	92.5	29	25	ABZ66523	Human HER2 synthe
18	14.8	92.5	29	25	ABZ66528	Human HER2 synthe
19	14.8	92.5	29	25	ABZ66529	Human HER2 synthe
20	14.8	92.5	29	25	ABZ66549	Human HIV enzymati
21	14.8	92.5	29	25	ABZ66550	Human HIV enzymati
22	14.8	92.5	29	25	ABZ66551	Human HIV enzymati
23	14.8	92.5	29	25	ABZ66552	Human HIV enzymati
24	14.8	92.5	29	25	ABZ66553	Human HIV enzymati
25	14.8	92.5	29	25	ABX13988	Deoxy-ribozyme, c1
26	14.8	92.5	29	25	ABX13989	Deoxy-ribozyme, c1
27	14.8	92.5	29	25	ABX13990	Deoxy-ribozyme, c1
28	14.8	92.5	29	25	ABX13991	Deoxy-ribozyme, c1
29	14.8	92.5	29	25	ABX13992	Deoxy-ribozyme, c1
30	14.8	92.5	29	25	ABX13993	Deoxy-ribozyme, c1
31	14.8	92.5	29	25	ABX13994	Deoxy-ribozyme, c1
32	14.8	92.5	29	25	ABX13995	Deoxy-ribozyme, c1
33	14.8	92.5	29	25	ABX13996	Deoxy-ribozyme, c1
34	14.8	92.5	29	25	ABX13997	Deoxy-ribozyme, c1
35	14.8	92.5	29	25	ABX13998	Deoxy-ribozyme, c1
36	14.8	92.5	29	25	ABX13999	Deoxy-ribozyme, c1
37	14.8	92.5	29	25	ABX14001	Deoxy-ribozyme, c1
38	14.8	92.5	29	25	ABX14002	Deoxy-ribozyme, c1
39	14.8	92.5	30	21	AAZ14525	Oligonucleotide 5'
40	14.8	92.5	30	21	AAZ27648	Human short protei
41	14.8	92.5	30	22	AAZ62302	Synthetic oligodeo
42	14.8	92.5	30	25	ACA10089	Necrosis factor ka
43	14.8	92.5	30	25	ACA10090	Necrosis factor ka
44	14.8	92.5	30	25	ACA10091	Necrosis factor ka
45	14.8	92.5	30	25	ACA10092	Necrosis factor ka
46	14.8	92.5	30	25	ACA10093	Necrosis factor ka
47	14.8	92.5	30	25	ABX14000	Deoxy-ribozyme, c1
48	14.8	92.5	31	20	AAZ24353	Nucleic acid-based
49	14.8	92.5	31	20	AAZ24380	Nucleic acid-based
50	14.8	92.5	31	20	AAZ24383	Nucleic acid-based
51	14.8	92.5	31	20	AAZ24386	Nucleic acid-based
52	14.8	92.5	31	20	AAZ24389	Nucleic acid-based
53	14.8	92.5	31	20	AAZ24393	Nucleic acid-based
54	14.8	92.5	31	20	AAZ21117	DNAzyme D23a nucle
55	14.8	92.5	31	21	AAZ52572	HCV RNA-binding c1
56	14.8	92.5	31	21	AAZ91150	HPV mRNA-cleaving
57	14.8	92.5	31	22	ABZ02611	HPV6 targeted DNA
58	14.8	92.5	31	22	ABZ02642	HPV16 targeted DNA
59	14.8	92.5	31	22	ABZ02643	HPV16 targeted DNA
60	14.8	92.5	31	22	ABZ02644	HPV16 targeted DNA
61	14.8	92.5	31	22	ABZ02645	HPV16 targeted DNA
62	14.8	92.5	31	22	ABZ02646	HPV16 targeted DNA
63	14.8	92.5	31	22	ABZ02647	HPV16 targeted DNA
64	14.8	92.5	31	22	ABZ02648	HPV16 targeted DNA
65	14.8	92.5	31	22	ABZ02649	HPV16 targeted DNA
66	14.8	92.5	31	22	ABZ02650	HPV16 targeted DNA
67	14.8	92.5	31	22	ABZ02651	HPV16 targeted DNA
68	14.8	92.5	31	22	ABZ02652	HPV11 targeted DNA
69	14.8	92.5	31	22	ABZ02653	HPV11 targeted DNA
70	14.8	92.5	31	22	ABZ02654	HPV11 targeted DNA
71	14.8	92.5	31	22	ABZ02655	HBV targeted DNA
72	14.8	92.5	31	22	ABZ02657	HBV targeted DNA
73	14.8	92.5	31	22	ABZ02658	HBV targeted DNA
74	14.8	92.5	31	22	ABZ02659	HBV targeted DNA
75	14.8	92.5	31	22	AAH96952	Human Chk1 ribozym
76	14.8	92.5	31	22	AAH96953	Human Chk1 ribozym
77	14.8	92.5	31	22	AAH96954	Human Chk1 ribozym
78	14.8	92.5	31	22	AAH96955	Human Chk1 ribozym
79	14.8	92.5	31	22	AAH96956	Human Chk1 ribozym
80	14.8	92.5	31	22	AAH96957	Human Chk1 ribozym
81	14.8	92.5	31	22	AAH96958	Human Chk1 ribozym













958	14.8	92.5	31	23	ABK06476	Human NOGO DNAzyme
959	14.8	92.5	31	23	ABK06477	Human NOGO DNAzyme
960	14.8	92.5	31	23	ABK06478	Human NOGO DNAzyme
961	14.8	92.5	31	23	ABK06479	Human NOGO DNAzyme
962	14.8	92.5	31	23	ABK06480	Human NOGO DNAzyme
963	14.8	92.5	31	23	ABK06481	Human NOGO DNAzyme
964	14.8	92.5	31	23	ABK06482	Human NOGO DNAzyme
965	14.8	92.5	31	23	ABK06483	Human NOGO DNAzyme
966	14.8	92.5	31	23	ABK06484	Human NOGO DNAzyme
967	14.8	92.5	31	23	ABK06485	Human NOGO DNAzyme
968	14.8	92.5	31	23	ABK06486	Human NOGO DNAzyme
969	14.8	92.5	31	23	ABK06487	Human NOGO DNAzyme
970	14.8	92.5	31	23	ABK06488	Human NOGO DNAzyme
971	14.8	92.5	31	23	ABK06489	Human NOGO DNAzyme
972	14.8	92.5	31	23	ABK06490	Human NOGO DNAzyme
973	14.8	92.5	31	23	ABK06491	Human NOGO DNAzyme
974	14.8	92.5	31	23	ABK06492	Human NOGO DNAzyme
975	14.8	92.5	31	23	ABK06493	Human NOGO DNAzyme
976	14.8	92.5	31	23	ABK06494	Human NOGO DNAzyme
977	14.8	92.5	31	23	ABK06495	Human NOGO DNAzyme
978	14.8	92.5	31	23	ABK06496	Human NOGO DNAzyme
979	14.8	92.5	31	23	ABK06497	Human NOGO DNAzyme
980	14.8	92.5	31	23	ABK06498	Human NOGO DNAzyme
981	14.8	92.5	31	23	ABK06499	Human NOGO DNAzyme
982	14.8	92.5	31	23	ABK06500	Human NOGO DNAzyme
983	14.8	92.5	31	23	ABK06501	Human NOGO DNAzyme
984	14.8	92.5	31	23	ABK06502	Human NOGO DNAzyme
985	14.8	92.5	31	23	ABK06503	Human NOGO DNAzyme
986	14.8	92.5	31	23	ABK06504	Human NOGO DNAzyme
987	14.8	92.5	31	23	ABK06505	Human NOGO DNAzyme
988	14.8	92.5	31	23	ABK06506	Human NOGO DNAzyme
989	14.8	92.5	31	23	ABK06507	Human NOGO DNAzyme
990	14.8	92.5	31	23	ABK06508	Human NOGO DNAzyme
991	14.8	92.5	31	23	ABK06509	Human NOGO DNAzyme
992	14.8	92.5	31	23	ABK06510	Human NOGO DNAzyme
993	14.8	92.5	31	23	ABK06511	Human NOGO DNAzyme
994	14.8	92.5	31	23	ABK06512	Human NOGO DNAzyme
995	14.8	92.5	31	23	ABK06513	Human NOGO DNAzyme
996	14.8	92.5	31	23	ABK06514	Human NOGO DNAzyme
997	14.8	92.5	31	23	ABK06515	Human NOGO DNAzyme
998	14.8	92.5	31	23	ABK06516	Human NOGO DNAzyme
999	14.8	92.5	31	23	ABK06517	Human NOGO DNAzyme
1000	14.8	92.5	31	25	AA153699	Prostate cancer ma

## ALIGNMENTS

RESULT 1  
AAV82954  
ID AAV82954 standard; DNA; 16 BP.

XX AAV82954;  
AC  
XX  
DT 05-MAR-1999 (first entry)  
XX  
DE Enzymatic DNA core motif region 10-23.  
XX  
KW Enzyme; catalysis; cleavage; target; pharmaceutical; medical; substrate;  
KW regulator; detergent; dental hygiene; meat tenderiser; ss.  
XX  
OS Synthetic.  
XX  
PN WO9849346-A1.  
XX  
PD 05-NOV-1998.  
XX  
PF 29-APR-1998; 98WO-US08677.  
XX  
PR 29-APR-1997; 97US-0045228.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX

PI Breaker RR, Joyce GF;  
XX  
DR WPI; 1999-034670/03.  
XX  
PT New catalytic DNA molecules - having site-specific endonuclease  
PT activity in a substrate nucleic acid, used for cleaving target  
PT nucleic acid sequences  
XX  
PS Claim 1; Page 96; 161pp; English.

This sequence is used in a method which involves the production of catalytic DNA molecules which can be used for cleaving target nucleic acid molecules. Such DNA molecules can be used in pharmaceutical and medical products (e.g. for wound debridement, clot dissolution), as well as in household items (e.g. detergents, dental hygiene products, meat tenderisers). Other suitable substrates include those comprising or produced by picornaviruses, hepadnaviridae (e.g. HBV, HCV), papillomaviruses (e.g. HPV), gammaherpesvirinae (e.g. EBV), lymphocryptoviruses, leukemia viruses (e.g. HTLV-1 and -II), flaviviruses, togaviruses, herpesviruses (including alphaherpesvirus and betaherpesviruses), cytomegaloviruses (CMV), influenza viruses, CC viruses and retroviruses contributing to immunodeficiency diseases and syndromes (e.g. HIV-1 and -2), simian and feline immunodeficiency viruses and bovine leukemia viruses. They can also be used as regulators of gene expression.

Sequence 16 BP; 5 A; 4 C; 4 G; 1 T; 2 other;

Query Match 92.5%; Score 14.8; DB 20; Length 16;  
Best local similarity 100.0%; Pred. No. 89;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGCGTAGCHACACGA 16  
DB 1 RGGCTAGCHACACGA 16

RESULT 2  
AAV82953  
ID AAV82953 standard; DNA; 16 BP.

XX AAV82953;  
AC  
XX  
DT 05-MAR-1999 (first entry)  
XX  
DE Enzymatic DNA core motif region.  
XX  
KW Enzyme; catalysis; cleavage; target; pharmaceutical; medical; substrate;  
KW regulator; detergent; dental hygiene; meat tenderiser; ss.  
XX  
OS Synthetic.  
XX  
PN WO9849346-A1.  
XX  
PD 05-NOV-1998.  
XX  
PF 29-APR-1998; 98WO-US08677.  
XX  
PR 29-APR-1997; 97US-0045228.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Breaker RR, Joyce GF;  
XX  
DR WPI; 1999-034670/03.  
XX  
PT New catalytic DNA molecules - having site-specific endonuclease  
PT activity in a substrate nucleic acid, used for cleaving target  
PT nucleic acid sequences  
XX  
PS Claim 1; Page 96; 161pp; English.  
XX  
CC This sequence is used in a method which involves the production of



DE	DNAzyme motif SEQ ID NO 21.
KV	Nucleic acid sensor molecule; detection; infection; disease diagnosis;
KW	nucleic acid abnormality; electronic; signalling molecule; ribozyme;
KX	nucleoside analogue; DNAzyme; ss.
OS	Synthetic.
PN	WO200166721-A2.
XX	
PD	13-SEP-2001.
PF	06-MAR-2001; 2001WO-US07163.
PR	06-MAR-2000; 2000US-187128P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PI	Usman N, McSwiggan JA, Zinnen S, Seiwert S, Haerberli P,
PI	Chowrira B, Blatt L;
DR	WPI; 2001-616242/71.
XX	
PT	New nucleic acid sensor molecule useful in diagnostic applications,
PT	nucleic acid-based electronics and functional genomics, comprises an
PS	enzymatic nucleic acid and one or more sensors -
PS	Disclosure; Fig 4; 115pp; English.
XX	
CC	The invention relates to a nucleic acid sensor molecule (I) comprising an
CC	enzymatic nucleic acid component and one or more sensor components. (I)
CC	is useful in diagnostic applications to identify the presence of genes
CC	and/or gene products indicative of a particular genotype and/or
CC	phenotype, e.g. a disease state or infection and for diagnosis of disease
CC	states or physiological abnormalities related to the expression of viral,
CC	bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based
CC	electronics, for the detection of specific target signalling molecules,
CC	in assays to assess the specificity, toxicity and effectiveness of
CC	various small molecules, nucleoside analogues or non-nucleic acid drugs
CC	or for detection of pathogens, biochemicals, organic or inorganic
CC	compounds. The present sequence is that of a DNAzyme motif of the
CC	invention.
SO	Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
QY	
DB	1 RGGCTAGGACAAACA 16      : 1 RGGCTAGGCTCAACA 16
XX	
RESULT 6	
AAH97756	
ID	AAH97756 standard; DNA; 16 BP.
XX	
AAH97756;	
XX	
DT	09-OCT-2001 (first entry)
XX	
DE	DNAzyme ribozyme motif SEQ ID NO: 3186.
XX	
KM	Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
KW	RNA cleavage; cancer; ss.
XX	
OS	Unidentified.
XX	
PN	WO200157206-A2.
XX	
DD	09-AUG-2001.
XX	

PF	02-FEB-2001; 2001WO-US03504.
XX	
PR	03-FEB-2000; 2000US-0179983.
XX	
XX	(RIBO-) RIBOZYME PHARM INC.
PA	(FATT/) FATTLEY A R.
XX	
XX	Fattaey AR, Jarvis T, McSwigen J, Booher RN, Holman PS,
PI	WPI, 2001-496922/54.
DR	
XX	
XX	Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
PT	molecules, which downregulate expression of a checkpoint kinase-1
PT	gene, useful for treating colorectal, lung, breast or prostate cancers
PT	
XX	
PS	Claim 8; Fig 5; 115pp; English.
XX	
CC	The present invention provides nucleic acid molecules capable of
CC	downregulating the expression of the human checkpoint kinase-1 (Chk1)
CC	gene. These may be antisense or ribozyme sequences, and are useful in the
CC	treatment of diseases associated with conditions affected by Chk1 levels,
CC	including cancer. The present sequence is an oligonucleotide described in
CC	the exemplification of the invention.
XX	
XX	Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
SO	
Query Match	92.5%; Score 14.8; DB 22; Length 16;
Best Local Similarity	93.8%; Pred. No. 89;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0.	
OY	1 RGCGTAGCHACACGA 16
	:
DB	1 RGCGTAGCTACACGA 16
RESULT 7	
ID	ABK09278
XX	ABK09278 standard; DNA; 16 BP.
XX	
AC	ABK09278;
XX	
DT	12-MAR-2002 (first entry)
XX	
XX	DNzyme motif.
XX	
XX	Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;
XX	cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW	muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW	DNzyme; inozyme; G-clavier; amberzyme; zinczyme; lymphoma; leukaemia;
KW	B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW	human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW	MCI; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW	inflammatory arthropathy; central nervous system injury;
KW	chemobrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW	chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW	Parkinson's disease; ataxia; Huntington's disease;
KW	Creutzfeldt-Jakob disease; macular dystrophy; neurodegenerative disease.
XX	
OS	Synthetic.
XX	
PN	WO200159103-A2.
XX	
PD	16-AUG-2001.
XX	
PF	09-FEB-2001; 2001WO-US04273.
XX	
PR	11-FEB-2000; 2000US-181797P.
PR	28-FEB-2000; 2000US-18516P.
PR	06-MAR-2000; 2000US-187128P.
XX	
XX	(RIBO-) RIBOZYME PHARM INC.
PA	(BLAT/) BLATT L.

PA (MCSW/J) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 P1 Blatt L, McSwiggen J, Chowrira BM;  
 XX  
 DR WPI, 2001-607195/69.  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,  
 PT and central nervous system injury -  
 PS  
 XX Disclosure; Fig 5; 200p; English.  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOCO).  
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN  
 CC motif) or an amberzyme (cleaving RNA with an NCH triplet), a zinczyme  
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used  
 CC to cleave RNA of CD20 in the presence of a divalent cation that is  
 CC preferably Mg<sup>2+</sup>. Furthermore, it may be contacted with a cell to reduce  
 CC CD20 activity of the cell and treat a patient having a condition  
 CC associated with the level of CD20. The treatment may further comprise the  
 CC use of one or more therapies. In particular, the CD20 targeting  
 CC nucleic acid may be used to treat lymphoma, leukemia, B-cell  
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky  
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human  
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),  
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune  
 CC thrombocytopenia, and inflammatory arthropathy. The NOCO-targeting  
 CC nucleic acid is used to cleave RNA of the NOCO gene in the presence of a  
 CC divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the nucleic acid  
 CC may be contacted with a cell to reduce NOCO activity of the cell and  
 CC treat a patient having a condition associated with the level of NOCO. The  
 CC treatment may further comprise the use of one or more therapies.  
 CC In particular, the NOCO-targeting nucleic acid may be used to treat  
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,  
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOCO expression. The  
 CC present sequence is a DNAzyme molecule of the invention.  
 CC  
 XX  
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 QY Query Match 92.5%; Score 14.8; DB 23; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 89;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 RGGCTAGCHACACGA 16  
 1 RGGCTAGCTACACGA 16  
 Db

XX  
 OS Homo sapiens.  
 XX  
 EN WO200211674-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 09-AUG-2001; 2001WO-US24970.  
 XX  
 PR 09-AUG-2000; 2000US-224383P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (SYNT) SYNTEX USA LLC.  
 PA (THOM/) THOMPSON J.  
 XX  
 P1 Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;  
 P1 Grape A;  
 XX  
 DR WPI, 2002-217145/27.  
 XX  
 CC The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention.  
 CC  
 XX  
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 QY Query Match 92.5%; Score 14.8; DB 24; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 89;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 RGGCTAGCHACACGA 16  
 1 RGGCTAGCTACACGA 16  
 Db

RESULT 8  
 ABR61076  
 ID ABR61076 standard; DNA; 16 BP.  
 AC ABR61076;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Human CLCA1 gene enzymatic nucleic acid #5445.  
 XX  
 KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KW acetylcysteine.

RESULT 9  
 ABR22719  
 ID ABR22719 standard; RNA; 16 BP.  
 AC ABR22719;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE DNAzyme motif.  
 XX  
 KW Human; hammerhead ribozyme; cytosolic; antitumor; antidiabetic;  
 KW ophthalmological; antirheumatic; antiproliferative; virucide; osteopathic;  
 KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;  
 KW Sturge Weber syndrome; Kipfel-Trenauay-Weber syndrome; leukemia; ss;  
 KW Osler-Weber-rendu syndrome; leukemia; osteoporosis; DNAzyme; inozyme;

KW amberzyme.  
 XX Synthetic.  
 OS  
 XX WO20018124-A2.  
 XX  
 XX 22-NOV-2001.  
 XX  
 XX 16-MAY-2001; 2001WO-US15866.  
 XX  
 XX 16-MAY-2000; 2000US-0572021.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (GLAXO) GLAXO GROUP LTD.  
 XX  
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;  
 PI WPI; 2002-082995/11.  
 DR  
 XX Novel polynucleotide which down regulates expression of Bts-related  
 PT gene, useful for treating cancer, diabetic retinopathy, macular  
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber  
 PT syndrome -  
 XX  
 XX Disclosure; Figure 5; 149pp; English.  
 PS  
 CC The invention relates to a nucleic acid molecule (I) which down regulates  
 CC expression of an Ets-related gene (ERG). (I) is useful for treating  
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 CC tumor angiosarcoma, diabetic retinopathy, macular degeneration, verruca  
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge  
 CC Weber syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-rendu  
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 CC treating a patient having a condition associated with the level of ERG,  
 CC by contacting cells of the patient with (I) under conditions suitable for  
 CC the treatment. The method comprises the use of one or more therapies  
 CC under conditions suitable for the treatment. Leukaemia or tumour  
 CC angiogenesis is treated by administering (I) to the patient in  
 CC conjunction with one or more of other therapies such as radiation or  
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 CC cation such as Mg<sup>2+</sup>. (I) is useful for diagnosis of conditions and  
 CC diseases related to the expression of ERG, and as diagnostic tool to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of ERG RNA in a cell. (I) is useful for specifically  
 CC targeting genes that share homology with ERG gene or ERG fusion genes.  
 CC ABK7354-ABK2719 represent nucleic acids, including antisense and  
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
 CC related PCR primers of the invention.  
 CC  
 XX  
 XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 SQ  
 Query Match 92.5%; Score 14.8; DB 24; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 89;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGGCTAGCHACACGA 16  
 1 |||||  
 DB 1 RGGCTAGCTACACGA 16  
 RESULT 10  
 ACA10109  
 ID ACA10109 standard; DNA; 16 BP.  
 XX  
 XX ACA10109;  
 AC  
 XX 03-JUN-2003 (first entry)  
 XX DT  
 XX Necrosis factor kappa B (NFkB) modulating DNazyme motif.  
 DB  
 XX

KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection;  
 KW  
 XX  
 XX Synthetic.  
 OS  
 XX US2002177568-A1.  
 XX  
 XX 28-NOV-2002.  
 XX  
 XX 23-MAY-2001; 2001US-0864785.  
 XX  
 XX 15-AUG-1994; 94US-0291932.  
 XX 07-DEC-1992; 92US-0987132.  
 XX 18-MAY-1994; 94US-0245466.  
 XX 23-DEC-1996; 96US-0777916.  
 XX  
 XX (STIN)/ STINCHOMB D T.  
 XX (MCSW)/ MCSWIGGEN J.  
 XX (DRAP)/ DRAPER K G.  
 XX  
 XX Stinchcomb DT, Mcswiggen J, Draper KG;  
 PI WPI; 2003-340953/32.  
 DR  
 XX Novel enzymatic nucleic acid molecules which down regulates expression  
 PT of a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases -  
 PT  
 XX  
 XX Fig 4; SEQ ID NO 3928; 72pp; English.  
 PS  
 CC The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents a motif of an enzymatic nucleic acid  
 CC used to modulate the function of a necrosis factor kappa B sub-unit.  
 CC  
 XX  
 XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 SQ  
 Query Match 92.5%; Score 14.8; DB 25; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 89;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGGCTAGCHACACGA 16  
 1 |||||  
 DB 1 RGGCTAGCTACACGA 16

OY 1 RGGCTAGCHACACGA 16  
|||:|||||  
Db 1 RGGCTAGCTACACGA 16

## RESULT 11

ID AB258432 standard; DNA; 16 BP.

AC AB258432;

DT 08-MAY-2003 (first entry)

DE DNazyme motif.

KM DNazyme; enzymatic nucleic acid; enzyme; transporter; drug  
KW delivery; cytosolic; virucide; gene therapy; ss.

OS Synthetic.

XX WO2003008628-A2.

XX 30-JAN-2003.

XX 22-JUL-2002; 2002WO-US23324.

XX 20-JUL-2001; 2001US-306995P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Beigelman L, Azharyev A, Azharyeva E;

XX WPI; 2003-247828/25.

PT New transporter compounds useful for delivering molecules into  
PT biological system such as cells, and for treating cancer and viral  
PT infections -

PS Disclosure; Fig 4; 88pp; English.

XX The present sequence is an example of a DNazyme, an enzymatic  
CC nuclear acid (ENA) that does not require the presence of a 2'-OH  
CC group for its activity. DNazymes can be used as the ENA moiety in  
CC novel ENA peptide conjugates (I) of the invention that facilitate  
CC delivery of molecules into biological systems, such as cells. The  
CC peptide part of the conjugate is typically a fusogenic peptide such  
CC as a peptide given in ABP72298-ABP72305. The conjugates can be  
CC used to treat a cancer patient, where the cancer is breast, lung,  
CC colorectal, brain, oesophageal, stomach, bladder, pancreas, cervix,  
CC head and neck or ovary cancer, melanoma, lymphoma, glioma or  
CC multidrug resistant cancer, or to treat a virus infection, where  
CC the virus is HIV, hepatitis B virus, hepatitis C virus,  
CC cytomegalovirus, Rous sarcoma virus, herpes simplex virus,  
CC poliovirus, influenza virus, rhinovirus, west nile virus, Ebola  
CC virus, foot and mouth disease virus or papilloma virus (all  
CC claimed). (I) are useful for introducing nucleotides,  
CC nucleosides, nucleic acid molecules, lipids, peptides, proteins  
CC and/or non-nucleosidic small molecules into a cell and to detect  
CC the presence of a target molecule in a biological system such as  
CC tissue, cell or cell lysate. They are useful as diagnostic tools  
CC to examine genetic drift and mutations within diseased cells or to  
CC detect the presence of a disease-related RNA in a cell.

XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;

Query Match 92.5%; Score 14.8; DB 25; Length 16;

Best Local Similarity 93.8%; Pred. No. 89;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
|||:|||||  
Db 1 RGGCTAGCTACACGA 16

## RESULT 12

ID AB266525 standard; RNA; 27 BP.

AC AB266525;

DT 21-MAR-2003 (first entry)

DE Human HER2 synthetic DNazyme #1.

KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;  
KW anti-thematic; cancer; AIDS; ss.

OS Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

XX 06-JUN-2001; 2001US-296249P.

XX 10-SEP-2001; 2001US-318471P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Mcswiggen J;

XX WPI; 2003-140484/13.

PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX Claim 3; Page 153; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosolic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,  
CC AB266525 - AB266529, AB266586 - AB266558 represent human ribozymes of the  
CC invention.

XX Sequence 27 BP; 6 A; 6 C; 10 G; 2 T; 3 U; 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 27;

Best Local Similarity 87.5%; Pred. No. 92;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
|||:|||||  
Db 6 AGGCTAGCTACACGA 21

## RESULT 13

ID AB266527 standard; RNA; 27 BP.

AC AB266527;

DT 21-MAR-2003 (first entry)

XX Human HER2 synthetic DNazyme #3.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;  
 KM anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 PD  
 XX 05-DEC-2002.  
 PD  
 XX 29-MAY-2002; 2002WO-US16840.  
 XX  
 XX 29-MAY-2001; 2001US-294140P.  
 PR 06-JUN-2001; 2001US-296249P.  
 PR 10-SEP-2001; 2001US-318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PL Mcswiggen J;  
 PI  
 DR WPI; 2003-140484/13.  
 XX  
 XX Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
 PS  
 XX Claim 3; Page 153; 185pp; English.  
 XX  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytosolic, anti-HIV, and  
 CC anti-rheumatic activity. The nucleic acid molecules are useful for  
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
 CC acids are also useful for treating breast, ovarian, colorectal, lung,  
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
 CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,  
 CC AB266525 - AB266529, AB266586 - AB266658 represent human ribozymes of the  
 CC invention.  
 XX  
 SQ Sequence 27 BP; 11 A; 8 C; 6 G; 2 T; 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 27;  
 Best Local Similarity 87.5%; Pred. No. 92;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGCHACACGA 16  
 :|||||:|||||  
 Db 6 AGGCTAGCTACACGA 21

RESULT 14  
 AA234361  
 ID AA234361 standard; DNA; 29 BP.  
 XX  
 AC AA234361;  
 XX  
 DT 14-DEC-1999 (first entry)  
 XX  
 DE Nucleic acid-based diagnostic exemplification oligonucleotide #23.  
 XX  
 KW Catalytic nucleic acid-based diagnostic method; determination; AIDS;  
 KM mutation; ribozyme; target; cleavage; amplification; PCR primer;  
 KM probe; cancer; human immune deficiency virus; cystic fibrosis; HIV; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9950452-A1.  
 XX  
 PD 07-OCT-1999.  
 XX

PR 16-MAR-1999; 99WO-IB00848.  
 XX  
 XX 27-MAR-1998; 98US-0079651.  
 PR  
 XX (JOHU) JOHNSON & JOHNSON RES PTY LTD.  
 PA  
 XX Todd AV, Fuery CJ, Cairns MJ;  
 PI  
 XX WPI; 1999-591332/50.  
 DR  
 XX  
 XX Detecting diseases associated with a known mutation by amplification  
 PT and cleavage with catalytic nucleic acids, particularly for cancer,  
 PT human immune deficiency virus and cystic fibrosis -  
 PS  
 XX Disclosure; Page 20; 57pp; English.  
 XX  
 CC The present invention describes a method for determining whether a  
 CC subject is afflicted with a disorder characterised by the presence of  
 CC a known nucleic acid. The method comprises: (i) amplifying, in an  
 CC isolated sample from the subject, the nucleic acid segment that, in an  
 CC affected individual contains (A), (ii) treating the amplicons with a  
 CC catalytic nucleic acid (I) that specifically recognizes and cleaves a  
 CC target sequence present in either the mutated or wild-type segments,  
 CC but not in both; and (iii) detecting any cleavage caused by (I). Step  
 CC (ii) may be performed concurrently with (i). The method is specifically  
 CC used to diagnose cancer (especially), acquired immune deficiency  
 CC syndrome and cystic fibrosis. (I) recognises as few as two bp to create  
 CC a cleavage site (contrast at least 4 bp required by enzymes used in  
 CC restriction fragment length polymorphism (RFLP) analysis); such sites  
 CC occur more frequently than restriction enzyme sites, and mismatched  
 CC primers can be used to induce cleavage sites for (I). The method is  
 CC potentially more flexible than RFLP and does not require any enzymes or  
 CC toxic compounds. AA234339 to AA234450 represent oligonucleotide  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 29 BP; 10 A; 5 C; 10 G; 3 T; 1 other;

Query Match 92.5%; Score 14.8; DB 20; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGCHACACGA 16  
 :|||||:|||||  
 Db 8 AGGCTAGCTACACGA 23

RESULT 15  
 AA234363  
 ID AA234363 standard; DNA; 29 BP.  
 XX  
 AC AA234363;  
 XX  
 DT 14-DEC-1999 (first entry)  
 XX  
 DE Nucleic acid-based diagnostic exemplification oligonucleotide #25.  
 XX  
 KW Catalytic nucleic acid-based diagnostic method; determination; AIDS;  
 KM mutation; ribozyme; target; cleavage; amplification; PCR primer;  
 KM probe; cancer; human immune deficiency virus; cystic fibrosis; HIV; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9950452-A1.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PR 16-MAR-1999; 99WO-IB00848.  
 XX  
 PR 27-MAR-1998; 98US-0079651.  
 XX  
 PA (JOHU) JOHNSON & JOHNSON RES PTY LTD.  
 XX  
 PI Todd AV, Fuery CJ, Cairns MJ;

XX DR WPI; 1999-591332/50.

XX PT Detecting diseases associated with a known mutation by amplification

XX PT and cleavage with catalytic nucleic acids, particularly for cancer,

XX PT human immune deficiency virus and cystic fibrosis -

XX PS Disclosure; Page 20; 57pp; English.

XX CC The present invention describes a method for determining whether a

XX CC subject is afflicted with a disorder characterized by the presence of

XX CC a known nucleic acid. The method comprises: (i) amplifying, in an

XX CC isolated sample from the subject, the nucleic acid segment that, in an

XX CC affected individual contains (A), (ii) treating the amplicons with a

XX CC catalytic nucleic acid (I) that specifically recognizes and cleaves a

XX CC target sequence present in either the mutated or wild-type segments,

XX CC but not in both; and (iii) detecting any cleavage caused by (I). Step

XX CC (ii) may be performed concurrently with (i). The method is specifically

XX CC used to diagnose cancer (especially), acquired immune deficiency

XX CC syndrome and cystic fibrosis. (i) recognizes as few as two bp to create

XX CC a cleavage site (contrast at least 4 bp required by enzymes used in

XX CC restriction fragment length polymorphism (RFLP) analysis); such sites

XX CC occur more frequently than restriction enzyme sites, and mismatched

XX CC primers can be used to induce cleavage sites for (I). The method is

XX CC potentially more flexible than RFLP and does not require any enzymes or

XX CC toxic compounds. AA23439 to AA234450 represent oligonucleotide

XX CC sequences used in the exemplification of the present invention.

XX SQ Sequence 29 BP; 7 A; 10 C; 5 G; 7 T; 0 other;

XX Query Match 92.5%; Score 14.8; DB 20; Length 29;

XX Best Local Similarity 87.5%; Pred. No. 93;

XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 RGCTAGCHACACGA 16

XX Db 9 AGCTAGCTACACGA 24

XX RESULT 16

XX AAC82623

XX ID AAC82623 standard; DNA; 29 BP.

XX AC AAC82623;

XX DT 13-MAR-2001 (first entry)

XX DE Hammerhead ribozyme DNA motif #23.

XX KW Detection; amplification; pathogenic bacteria; hammerhead ribozyme;

XX KW fluorescent signal; cleavage; ss.

XX OS Synthetic.

XX PN DE19915141-A1.

XX PD 28-SEP-2000.

XX PF 26-MAR-1999; 99DE-1015141.

XX PR 26-MAR-1999; 99DE-1015141.

XX PA (ARTU-) ARTUS GES MOLEKULARBIOLOGISCHE DIAGNOSTI.

XX PI Krupp G;

XX DR WPI; 2000-603196/58.

XX PT Real-time quantitative amplification of nucleic acid, useful for

XX PT detecting bacterial pathogens, uses primer and labeled probe that

XX PT combine to form a ribozyme -

XX PS Disclosure; Fig 13; 39pp; German.

XX CC This invention describes a novel method for the amplification and

XX CC quantitative real-time determination of nucleic acid (I) using a primer

XX CC attached to a 1-40 nucleotide sequence (II) in the transcription product.

XX CC Amplification is done in the presence of an excess, preferably 50-500 nM,

XX CC of a nucleic acid probe (III) and labeled by a reporter molecule and a

XX CC quencher molecule. (I) encodes the motif 5'-GAAA-3' (A), and (II)

XX CC contains the motif 5'-GUGANGA-3' (B). (III) has 25-60, especially 50,

XX CC nucleotides. The method is used to detect and quantify (I) from

XX CC pathogenic bacteria. The method allows real-time detection and

XX CC quantification of (I), particularly RNA by NASBA (RTM) (nucleic acid

XX CC sequence-based amplification), without the difficulties associated with

XX CC use of DNA probes (see Nucleic Acid Res., 26 (1998) 2150) and is suitable

XX CC for routine use. Specifically the combination of (A) and (B) generates a

XX CC hammerhead ribozyme that cleaves the probe and generates a fluorescent

XX CC signal. Since many probes are cleaved, a high signal is produced,

XX CC resulting in high sensitivity and shorter reaction times. The method is

XX CC very specific since exact hybridization of probe to target is necessary

XX CC for cleavage to occur. Complicated probes are not required because

XX CC cleavage results in dissociation of the probe from the target (which

XX CC allows multiplexing). Stable and inexpensive probes can be used,

XX CC consisting mainly of 2'-deoxyribonucleotides.

XX SQ Sequence 29 BP; 5 A; 4 C; 4 G; 2 T; 14 other;

XX Query Match 92.5%; Score 14.8; DB 21; Length 29;

XX Best Local Similarity 93.8%; Pred. No. 93;

XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 RGCTAGCHACACGA 16

XX Db 7 RGCTAGCTACACGA 22

XX RESULT 17

XX ABZ6526

XX ID ABZ6526 standard; RNA; 29 BP.

XX AC ABZ6526;

XX DT 21-MAR-2003 (first entry)

XX DE Human HER2 synthetic DNAAzyme #2.

XX KW Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;

XX KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US16840.

XX PR 29-MAY-2001; 2001US-294140P.

XX PR 06-JUN-2001; 2001US-296249P.

XX PR 10-SEP-2001; 2001US-318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswigen J;

XX DR WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for

XX PT treating cancer, modulates the expression of a nucleic acid encoding

XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX PS Claim 3; Page 153; 185pp; English.

XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosstatic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the  
CC invention.

XX SQ Sequence 29 BP; 11 A; 7 C; 7 G; 2 T; 2 U; 0 other;

XX Query Match 92.5%; Score 14.8; DB 25; Length 29;  
XX Best Local Similarity 87.5%; Pred. No. 93;  
XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACACGA 16  
:|||||:|||||:  
Db 7 AGGCTAGCTACACGA 22

RESULT 18  
ABZ66528  
ID ABZ66528 standard; RNA; 29 BP.  
AC ABZ66528;  
XX  
XX 21-MAR-2003 (first entry)  
XX  
XX Human HER2 synthetic DNAzyme #4.  
XX  
XX Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
XX anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200297114-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 29-MAY-2002; 2002WO-US16840.  
XX  
XX 29-MAY-2001; 2001US-294140P.  
XX 06-JUN-2001; 2001US-296249P.  
XX 10-SEP-2001; 2001US-318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswiggen J;  
XX  
XX WPI; 2003-140484/13.  
XX  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
XX treating cancer, modulates the expression of a nucleic acid encoding  
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX  
XX Claim 3; Page 153; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosstatic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the  
CC invention.

XX SQ Sequence 29 BP; 9 A; 5 C; 11 G; 2 T; 2 U; 0 other;

XX Query Match 92.5%; Score 14.8; DB 25; Length 29;  
XX Best Local Similarity 87.5%; Pred. No. 93;  
XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACACGA 16  
:|||||:|||||:  
Db 7 AGGCTAGCTACACGA 22

RESULT 19  
ABZ66529  
ID ABZ66529 standard; RNA; 29 BP.  
AC ABZ66529;  
XX  
XX 21-MAR-2003 (first entry)  
XX  
XX Human HER2 synthetic DNAzyme #5.  
XX  
XX Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
XX anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200297114-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 29-MAY-2002; 2002WO-US16840.  
XX  
XX 29-MAY-2001; 2001US-294140P.  
XX 06-JUN-2001; 2001US-296249P.  
XX 10-SEP-2001; 2001US-318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswiggen J;  
XX  
XX WPI; 2003-140484/13.  
XX  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
XX treating cancer, modulates the expression of a nucleic acid encoding  
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX  
XX Claim 3; Page 153; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosstatic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the  
CC invention.

XX SQ Sequence 29 BP; 7 A; 4 C; 11 G; 2 T; 5 U; 0 other;

XX Query Match 92.5%; Score 14.8; DB 25; Length 29;  
XX Best Local Similarity 87.5%; Pred. No. 93;  
XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACACGA 16  
:|||||:|||||:  
Db 7 AGGCTAGCTACACGA 22

RESULT 20  
AB266649 standard; RNA; 29 BP.  
XX  
AC AB266649;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Human HIV enzymatic nucleic acid #1.  
XX  
KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
XX anti-rheumatic; cancer; AIDS; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200297114-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 29-MAY-2002; 2002WO-US16840.  
XX  
PR 29-MAY-2001; 2001US-294140P.  
PR 06-JUN-2001; 2001US-296249P.  
PR 10-SEP-2001; 2001US-318471P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcwigen J;  
XX  
DR WPI; 2003-140484/13.  
XX  
PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX  
PS Claim 122; Page 159; 185pp; English.  
XX  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosstatic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,  
CC AB266525 - AB266529, AB266586 - AB266658 represent human ribozymes of the  
CC invention.  
XX  
SQ Sequence 29 BP; 7 A; 11 C; 5 G; 2 T; 4 U; 0 other;  
XX  
Query Match 92.5%; Score 14.8; DB 25; Length 29;  
Best Local Similarity 87.5%; Pred. No. 93;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RGGCTAGCHACACGA 16  
Db 7 AGGCTAGCTACACGA 22  
XX  
RESULT 21  
AB266650 standard; RNA; 29 BP.  
XX  
AC AB266650;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Human HIV enzymatic nucleic acid #2.  
XX

KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
KM anti-rheumatic; cancer; AIDS; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200297114-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 29-MAY-2002; 2002WO-US16840.  
XX  
PR 29-MAY-2001; 2001US-294140P.  
PR 06-JUN-2001; 2001US-296249P.  
PR 10-SEP-2001; 2001US-318471P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcwigen J;  
XX  
DR WPI; 2003-140484/13.  
XX  
PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX  
PS Claim 122; Page 159; 185pp; English.  
XX  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosstatic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,  
CC AB266525 - AB266529, AB266586 - AB266658 represent human ribozymes of the  
CC invention.  
XX  
SQ Sequence 29 BP; 7 A; 9 C; 5 G; 2 T; 6 U; 0 other;  
XX  
Query Match 92.5%; Score 14.8; DB 25; Length 29;  
Best Local Similarity 87.5%; Pred. No. 93;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RGGCTAGCHACACGA 16  
Db 7 GGGCTAGCTACACGA 22  
XX  
RESULT 22  
AB266651 standard; RNA; 29 BP.  
XX  
AC AB266651;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Human HIV enzymatic nucleic acid #3.  
XX  
KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200297114-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 29-MAY-2002; 2002WO-US16840.  
XX

XX 29-MAY-2001; 2001US-294140P.  
 PR 06-JUN-2001; 2001US-296249P.  
 PR 10-SEP-2001; 2001US-318471P.  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J;  
 DR WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
 PS Claim 122; Page 159; 185pp; English.  
 CC  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytosstatic, anti-HIV, and  
 CC anti-rheumatic activity. The nucleic acid molecules are useful for  
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
 CC acids are also useful for treating breast, ovarian, colorectal, lung,  
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
 CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the  
 CC invention.  
 XX  
 SQ Sequence 29 BP; 6 A; 9 C; 6 G; 2 T; 6 U; 0 other;  
 Query Match 92.5%; Score 14.8; DB 25; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGGCTAGCHACACGA 16  
 Db 7 AGGCTAGCTACACGA 22  
 RESULT 23  
 ABZ66652  
 ID ABZ66652 standard; RNA; 29 BP.  
 AC ABZ66652;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human HIV enzymatic nucleic acid #4.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US16840.  
 XX  
 PR 29-MAY-2001; 2001US-294140P.  
 PR 06-JUN-2001; 2001US-296249P.  
 PR 10-SEP-2001; 2001US-318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J;  
 DR WPI; 2003-140484/13.  
 XX

PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
 PS Claim 122; Page 159; 185pp; English.  
 CC  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytosstatic, anti-HIV, and  
 CC anti-rheumatic activity. The nucleic acid molecules are useful for  
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
 CC acids are also useful for treating breast, ovarian, colorectal, lung,  
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
 CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the  
 CC invention.  
 XX  
 SQ Sequence 29 BP; 8 A; 6 C; 8 G; 2 T; 5 U; 0 other;  
 Query Match 92.5%; Score 14.8; DB 25; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGGCTAGCHACACGA 16  
 Db 7 AGGCTAGCTACACGA 22  
 RESULT 24  
 ABZ66653  
 ID ABZ66653 standard; RNA; 29 BP.  
 AC ABZ66653;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human HIV enzymatic nucleic acid #5.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US16840.  
 XX  
 PR 29-MAY-2001; 2001US-294140P.  
 PR 06-JUN-2001; 2001US-296249P.  
 PR 10-SEP-2001; 2001US-318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J;  
 DR WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
 PS Claim 122; Page 159; 185pp; English.  
 CC  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytosstatic, anti-HIV, and

CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,  
CC AB265525 - AB265529, AB265586 - AB266658 represent human ribozymes of the  
CC invention.  
XX  
SQ Sequence 29 BP; 7 A; 12 C; 5 G; 2 T; 3 U; 0 other;  
Query Match 92.5%; Score 14.8; DB 25; Length 29;  
Best Local Similarity 87.5%; Pred. No. 93;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RGCTAGCHACACGA 16  
:|||||:|||||  
7 AGGCTAGTACACGA 22  
DB  
RESULT 25  
ABX13988 ID ABX13988 standard; DNA; 29 BP.  
XX  
AC ABX13988;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1594.  
XX  
KM Catalytic DNA; catalytic RNA; hairless protein; ss;  
KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KM catalytic core; cleavage site; pharmaceutical; hair production;  
KM hair follicle; anagen phase; catagen phase; hair removal product;  
KM depilatory.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 8..22  
FT /\*tag= a  
FT /note= "Catalytic domain"  
XX  
FN WO200283891-A2.  
XX  
PD 24-OCT-2002.  
XX  
PP 12-APR-2002; 2002WO-US11683.  
XX  
PR 13-APR-2001; 2001US-283618P.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Christiano AM;  
XX  
DR WPI; 2003-093020/08.  
XX  
PT New catalytic nucleic acid molecule that specifically cleaves Hairless  
PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
PT cell, or for inhibiting transition of a hair follicle from anagen phase  
PT to catagen phase -  
XX  
PS Claim 3; Page 34; 65pp; English.  
XX  
CC The invention discloses a new catalytic DNA or RNA molecule that  
CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
CC which comprises a catalytic domain that cleaves mRNA at a defined  
CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
CC of the catalytic domain. Lack of expression of the hairless gene due to  
CC inherited mutations leads to the complete loss of hair, known as  
CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
CC the genes promoting hair growth, and one way to get targeted, transient

CC gene suppression is through the use of catalytic nucleic acid technology,  
CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
CC a self-catalytic enzymatic function and sequence specific RNA binding  
CC ability. Small DNA oligonucleotides that have a similar structure to the  
CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
CC more lenient consensus cleavage site requirements and are less likely to  
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
CC are useful in pharmaceutical compositions for inhibiting hair production  
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
CC the transition of a hair follicle from the anagen phase to the catagen  
CC phase. A non-human transgenic mammal is useful as a model for testing  
CC hair removal products which function by inhibiting hairless protein  
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
CC human hairless protein mRNA immediately after nucleotide 1594.  
XX  
SQ Sequence 29 BP; 7 A; 10 C; 8 G; 4 T; 0 other;  
Query Match 92.5%; Score 14.8; DB 25; Length 29;  
Best Local Similarity 87.5%; Pred. No. 93;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RGCTAGCHACACGA 16  
:|||||:|||||  
7 GGGCTAGTACACGA 22  
DB  
RESULT 26  
ABX13989 ID ABX13989 standard; DNA; 29 BP.  
XX  
AC ABX13989;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1597.  
XX  
KM Catalytic DNA; catalytic RNA; hairless protein; ss;  
KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KM catalytic core; cleavage site; pharmaceutical; hair production;  
KM hair follicle; anagen phase; catagen phase; hair removal product;  
KM depilatory.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 8..22  
FT /\*tag= a  
FT /note= "Catalytic domain"  
XX  
FN WO200283891-A2.  
XX  
PD 24-OCT-2002.  
XX  
PP 12-APR-2002; 2002WO-US11683.  
XX  
PR 13-APR-2001; 2001US-283618P.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Christiano AM;  
XX  
DR WPI; 2003-093020/08.  
XX  
PT New catalytic nucleic acid molecule that specifically cleaves Hairless  
PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
PT cell, or for inhibiting transition of a hair follicle from anagen phase  
PT to catagen phase -  
XX  
PS Claim 3; Page 34; 65pp; English.  
XX

CC The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, hairless protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, *in vivo*, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 1597.  
 CC  
 SQ Sequence 29 BP; 7 A; 9 C; 10 G; 3 T; 0 other;  
 Query Match 92.5%; Score 14.8; DB 25; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGGCTAGGCHACACGA 16  
 Db 7 AGGCTAGGCTACACGA 22  
 RESULT 27  
 ABX13990  
 ID ABX13990 standard; DNA; 29 BP.  
 AC ABX13990;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1641.  
 KW Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
 KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
 KW catalytic core; cleavage site; pharmaceutical; hair production;  
 KW hair follicle; anagen phase; catagen phase; hair removal product;  
 KW depilatory.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 8..22  
 FT /\*tag= a  
 FT /note= "Catalytic domain"  
 FT  
 XX WO200283891-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 XX 12-APR-2002; 2002WO-US11683.  
 XX  
 XX 13-APR-2001; 2001US-283618P.  
 XX  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 FI Christiano AM;  
 FI  
 XX  
 DR WPI; 2003-093020/08.

XX  
 PT New catalytic nucleic acid molecule that specifically cleaves hairless  
 PT protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase  
 XX  
 PS Claim 3; Page 34; 65pp; English.  
 XX  
 CC The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, hairless protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, *in vivo*, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 1641.  
 CC  
 SQ Sequence 29 BP; 7 A; 11 C; 7 G; 4 T; 0 other;  
 Query Match 92.5%; Score 14.8; DB 25; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGGCTAGGCHACACGA 16  
 Db 7 AGGCTAGGCTACACGA 22  
 RESULT 28  
 ABX13991  
 ID ABX13991 standard; DNA; 29 BP.  
 AC ABX13991;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1698.  
 KW Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
 KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
 KW catalytic core; cleavage site; pharmaceutical; hair production;  
 KW hair follicle; anagen phase; catagen phase; hair removal product;  
 KW depilatory.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 8..22  
 FT /\*tag= a  
 FT /note= "Catalytic domain"  
 FT  
 XX WO200283891-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 XX 12-APR-2002; 2002WO-US11683.

XX 13-APR-2001; 2001US-283618P.  
 PR (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 XX Christiano AM;  
 XX WPI; 2003-093020/08.  
 DR  
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase -  
 XX  
 XX Claim 3; Page 34; 65pp; English.  
 XX  
 XX The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 1698.  
 CC  
 XX  
 SQ Sequence 29 BP; 7 A; 7 C; 10 G; 5 T; 0 other;  
 Query Match 92.5%; Score 14.8; DB 25; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
 :|||||:|||||  
 Db 7 AGGCTAGCTACACGA 22

RESULT 29  
 ABX13992  
 ID ABX13992 standard; DNA; 29 BP.  
 XX  
 AC ABX13992;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1732.  
 XX  
 KW Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
 KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
 KW catalytic core; cleavage site; pharmaceutical; hair production;  
 KW hair follicle; anagen phase; catagen phase; hair removal product;  
 KW depilatory.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 8..22

FT /\*tag= a  
 FT /note= "Catalytic domain"  
 EN W0200283891-A2.  
 XX  
 XX 24-OCT-2002.  
 PD  
 XX  
 PE 12-APR-2002; 2002WO-US11663.  
 XX  
 XX 13-APR-2001; 2001US-283618P.  
 ER (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 XX Christiano AM;  
 XX WPI; 2003-093020/08.  
 DR  
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase -  
 XX  
 XX Claim 3; Page 34; 65pp; English.  
 XX  
 XX The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 1732.  
 CC  
 XX  
 SQ Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;  
 Query Match 92.5%; Score 14.8; DB 25; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
 :|||||:|||||  
 Db 7 AGGCTAGCTACACGA 22

RESULT 30  
 ABX13993  
 ID ABX13993 standard; DNA; 29 BP.  
 XX  
 AC ABX13993;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1750.  
 XX  
 KW Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
 KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
 KW catalytic core; cleavage site; pharmaceutical; hair production;

KV	hair follicle; anagen phase; catagen phase; hair removal product;
XW	deplactory.
XX	Homo sapiens.
OS	Synthetic.
FH	Key Location/Qualifiers
FT	misc_feature 8..22 /tag= a
FT	/note= "Catalytic domain"
FN	WO200263891-A2.
PD	24-OCT-2002.
PX	12-APR-2002; 2002WO-US11683.
PR	13-APR-2001; 2001US-283618P.
PA	(UYCO ) UNITV COLUMBIA NEW YORK.
PI	Christiano AM;
DR	WPI; 2003-093020/08.
PT	New catalytic nucleic acid molecule that specifically cleaves Hairless Protein mRNA, useful for inhibiting hair production by a hair-producing cell, or for inhibiting transition of a hair follicle from anagen phase to catagen phase -
PS	Claim 3; Page 34; 65pp; English.
CC	The invention discloses a new catalytic DNA or RNA molecule that specifically cleaves, or inhibits expression of, Hairless protein mRNA which comprises a catalytic domain that cleaves mRNA at a defined consensus sequence and binding domains contiguous with the 5' and 3' ends of the catalytic domain. Lack of expression of the hairless gene due to inherited mutations leads to the complete loss of hair. Known as atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting the genes promoting hair growth, and one way to get targeted, transient CC gene suppression is through the use of catalytic nucleic acid technology, including ribozymes and DNazymes. Ribozymes are RNA structures which have CC a self-catalytic enzymatic function and sequence specific RNA binding ability. Small DNA oligonucleotides that have a similar structure to the hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a CC catalytic core and two sequence specific arms. The deoxy-ribozymes have more lenient consensus cleavage site requirements and are less likely to degrade. In vivo, that hammerhead ribozymes. The catalytic nucleic acids CC are useful in pharmaceutical compositions for inhibiting hair production by a hair-producing cell, for inhibiting hair growth and for inhibiting CC the transition of a hair follicle from the anagen phase to the catagen phase. A non-human transgenic mammal is useful as a model for testing CC hair removal products which function by inhibiting hairless protein expression. The sequence presented is the deoxy-ribozyme that cleaves the human hairless protein mRNA immediately after nucleotide 1750.
SC	Sequence 29 BP; 8 A; 9 C; 7 G; 5 T; 0 other;
OY	Query Match 92.5%; Score 14.8; DB 25; Length 29; Best Local Similarity 87.5%; Pred. No. 93; Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0.0;
ID	ABX13994 standard; DNA; 29 BP. ABX13994 AC CX
DB	1 RGGGTAGGACAACGA 16 ::   :   : 7 GGCGTAGCTAACACCA 22
RJ	RESULT 31 ID ABX13994 standard; DNA; 29 BP. AC CX

DT		25-FEB-2003	(first entry)
XX			
DE		Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1801.	
XX			
KM		Catalytic DNA; catalytic RNA; hairless protein; ss;	
KW		hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;	
KM		ribozyme; DNAszyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;	
KW		catalytic core; cleavage site; pharmaceutical; hair production;	
KM		hair follicle; anagen phase; catagen phase; hair removal product;	
KW		deplatory.	
XX			
OS	Homo sapiens.		
XX	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	misc_feature	8..22	
FT		/tag= a	
FT		/note= "Catalytic domain"	
PN			
PM	WO200283891-A2.		
PD			
PD	24-OCT-2002.		
PF			
PR	12-APR-2002; 2002MO-US11683.		
PA			
XX	13-APR-2001; 2001US-283618P.		
XX	(UYCO ) UNIV COLUMBIA NEW YORK.		
PI	Christiano AM;		
XX			
DR	WPI; 2003-093020/08.		
PT			
PT	New catalytic nucleic acid molecule that specifically cleaves Hairless		
PT	Protein mRNA, useful for inhibiting hair production by a hair-producing		
PT	cell, or for inhibiting transition of a hair-follicle from anagen phase		
XX	to catagen phase		
PS			
XX	Claim 3; Page 34; 65pp; English.		
CC			
CC	The invention discloses a new catalytic DNA or RNA molecule that		
CC	specifically cleaves, or inhibits expression of, Hairless Protein mRNA		
CC	which comprises a catalytic domain that cleaves mRNA at a defined		
CC	consensus sequence and binding domains contiguous with the 5' and 3' ends		
CC	of the catalytic domain. Lack of expression of the hairless gene due to		
CC	inherited mutations leads to the complete loss of hair, known as		
CC	atrachia. Abundant hair growth, hirsutism, can be improved by inhibiting		
CC	the genes promoting hair growth, and one way to get targeted, transient		
CC	gene suppression is through the use of catalytic nucleic acid technology,		
CC	including ribozymes and DNAszymes. Ribozymes are RNA structures which have		
CC	a self-catalytic enzymatic function and sequence specific RNA binding		
CC	ability. Small DNA oligonucleotides that have a similar structure to the		
CC	hammerhead ribozyme, called deoxy-ribozymes or DNAszymes, having a		
CC	catalytic core and two sequence specific arms. The deoxy-ribozymes have		
CC	more lenient consensus cleavage site requirements and are less likely to		
CC	degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids		
CC	are useful in pharmaceutical compositions for inhibiting hair production		
CC	by a hair-producing cell, for inhibiting hair growth and for inhibiting		
CC	the transition of a hair follicle from the anagen phase to the catagen		
CC	phase. A non-human transgenic mammal is useful as a model for testing		
CC	hair removal products which function by inhibiting hairless protein		
CC	expression. The sequence presented is the deoxy-ribozyme that cleaves the		
CC	human hairless protein mRNA immediately after nucleotide 1801.		
XX			
XX			
SO	Sequence 29 BP; 9 A; 6 C; 11 G; 3 T; 0 other;		
QY			
QY	Query Match	92.5%; Score 14.8; DB 25; Length 29;	
DB	Best Local Similarity	87.5%; Pred. NO. 93;	
DB	Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0		
DB			
DB	1 RGCGTACGCAACAAGA 16		
DB	:     :     :		
DB	7 AGCGTAGCTACAAACA 22		

RESULT 32  
ABX13995  
ID ABX13995 standard; DNA; 29 BP.  
AC  
XX  
XX  
ABX13995;  
XX  
XX  
25-FEB-2003 (first entry)  
XX  
XX  
Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1811.  
XX  
XX  
Catalytic DNA; catalytic RNA; hairless protein; ss;  
KW hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;  
KW ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KW catalytic core; cleavage site; pharmaceutical; hair production;  
KW hair follicle; anagen phase; catagen phase; hair removal product;  
KW deplatory.  
XX  
XX  
Homo sapiens.  
OS Synthetic.  
XX  
XX  
Key Location/Qualifiers  
FH misc\_feature 8..22  
FT /tag= a  
FT /note= "Catalytic domain"  
XX  
XX  
WO200283891-A2.  
XX  
XX  
24-OCT-2002.  
XX  
XX  
12-APR-2002; 2002WO-US11683.  
XX  
XX  
13-APR-2001; 2001US-283618P.  
XX  
XX  
(UNCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX  
Christiano AM;  
XX  
XX  
WPI; 2003-093020/08.  
XX  
XX  
New catalytic nucleic acid molecule that specifically cleaves Hairless  
PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
PT cell, or for inhibiting transition of a hair follicle from anagen phase  
PT to catagen phase -  
XX  
XX  
PS  
XX  
Claim 3; Page 35; 65pp; English.  
XX  
XX  
The invention discloses a new catalytic DNA or RNA molecule that  
CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
CC which comprises a catalytic domain that cleaves mRNA at a defined  
CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
CC of the catalytic domain. Lack of expression of the hairless gene due to  
CC inherited mutations leads to the complete loss of hair, known as  
CC atichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
CC the genes promoting hair growth, and one way to get targeted, transient  
CC gene suppression is through the use of catalytic nucleic acid technology,  
CC including ribozymes and DNzymes. Ribozymes are RNA structures which have  
CC a self-catalytic enzymatic function and sequence specific RNA binding  
CC ability. Small DNA oligonucleotides that have a similar structure to the  
CC hammerhead ribozyme, called deoxy-ribozymes or DNzymes, having a  
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
CC more lenient consensus cleavage site requirements and are less likely to  
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
CC are useful in pharmaceutical compositions for inhibiting hair production  
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
CC the transition of a hair follicle from the anagen phase to the catagen  
CC phase. A non-human transgenic mammal is useful as a model for testing  
CC hair removal products which function by inhibiting hairless protein  
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
CC human hairless protein mRNA immediately after nucleotide 1811.  
XX  
XX  
Sequence 29 BP; 9 A; 9 C; 9 G; 2 T; 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 29;  
Best Local Similarity 87.5%; Pred. No. 93;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGGCTAGGCAACCA 16  
:|||||:  
Db 7 AGGCTAGCTACCA 22  
RESULT 33  
ABX13996  
ID ABX13996 standard; DNA; 29 BP.  
AC  
XX  
XX  
ABX13996;  
XX  
XX  
25-FEB-2003 (first entry)  
XX  
XX  
Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2028.  
XX  
XX  
Catalytic DNA; catalytic RNA; hairless protein; ss;  
KW hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;  
KW ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KW catalytic core; cleavage site; pharmaceutical; hair production;  
KW hair follicle; anagen phase; catagen phase; hair removal product;  
KW deplatory.  
XX  
XX  
Homo sapiens.  
OS Synthetic.  
XX  
XX  
Key Location/Qualifiers  
FH misc\_feature 8..22  
FT /tag= a  
FT /note= "Catalytic domain"  
XX  
XX  
WO200283891-A2.  
XX  
XX  
24-OCT-2002.  
XX  
XX  
12-APR-2002; 2002WO-US11683.  
XX  
XX  
13-APR-2001; 2001US-283618P.  
XX  
XX  
(UNCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX  
Christiano AM;  
XX  
XX  
WPI; 2003-093020/08.  
XX  
XX  
New catalytic nucleic acid molecule that specifically cleaves Hairless  
PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
PT cell, or for inhibiting transition of a hair follicle from anagen phase  
PT to catagen phase -  
XX  
XX  
PS  
XX  
Claim 3; Page 35; 65pp; English.  
XX  
XX  
The invention discloses a new catalytic DNA or RNA molecule that  
CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
CC which comprises a catalytic domain that cleaves mRNA at a defined  
CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
CC of the catalytic domain. Lack of expression of the hairless gene due to  
CC inherited mutations leads to the complete loss of hair, known as  
CC atichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
CC the genes promoting hair growth, and one way to get targeted, transient  
CC gene suppression is through the use of catalytic nucleic acid technology,  
CC including ribozymes and DNzymes. Ribozymes are RNA structures which have  
CC a self-catalytic enzymatic function and sequence specific RNA binding  
CC ability. Small DNA oligonucleotides that have a similar structure to the  
CC hammerhead ribozyme, called deoxy-ribozymes or DNzymes, having a  
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
CC more lenient consensus cleavage site requirements and are less likely to  
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
CC are useful in pharmaceutical compositions for inhibiting hair production

CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
CC the transition of a hair follicle from the anagen phase to the catagen  
CC phase. A non-human transgenic mammal is useful as a model for testing  
CC hair removal products which function by inhibiting hairless protein  
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
CC human hairless protein mRNA immediately after nucleotide 2028.  
CC  
XX  
SQ Sequence 29 BP; 6 A; 7 C; 13 G; 3 T; 0 other;  
Query Match 92.5%; Score 14.8; DB 25; Length 29;  
Best Local Similarity 87.5%; Pred. No. 93;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGGCTAGCHACACGA 16  
Db 7 GGGCTAGCTACACGA 22  
RESULT 34  
ID ABX13997  
AC ABX13997 standard; DNA; 29 BP.  
XX  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2033.  
XX  
XX Catalytic DNA; catalytic RNA; hairless protein; ss;  
KM hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;  
KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KM catalytic core; cleavage site; pharmaceutical; hair production;  
KM hair follicle; anagen phase; catagen phase; hair removal product;  
KM depilatory.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH 8..22  
FT misc\_feature /tag= a  
FT /note= "Catalytic domain"  
XX  
XX WO200283891-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 12-APR-2002; 2002WO-US11683.  
XX  
XX 13-APR-2001; 2001US-283618P.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX Christiano AM;  
XX  
XX WPI; 2003-093020/08.  
XX  
XX  
XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
XX Protein mRNA, useful for inhibiting hair production by a hair-producing  
XX cell, or for inhibiting transition of a hair follicle from anagen phase  
XX to catagen phase -  
XX  
XX Claim 3; Page 35; 65pp; English.  
XX  
XX The invention discloses a new catalytic DNA or RNA molecule that  
XX specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
XX which comprises a catalytic domain that cleaves mRNA at a defined  
XX consensus sequence and binding domains contiguous with the 5' and 3' ends  
XX of the catalytic domain. Lack of expression of the hairless gene due to  
XX inherited mutations leads to the complete loss of hair, known as  
XX atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
XX the genes promoting hair growth, and one way to get targeted, transient  
XX gene suppression is through the use of catalytic nucleic acid technology.

CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
CC a self-catalytic enzymatic function and sequence specific RNA binding  
CC ability. Small DNA oligonucleotides that have a similar structure to the  
CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
CC more lenient consensus cleavage site requirements and are less likely to  
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
CC are useful in pharmaceutical compositions for inhibiting hair production  
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
CC the transition of a hair follicle from the anagen phase to the catagen  
CC phase. A non-human transgenic mammal is useful as a model for testing  
CC hair removal products which function by inhibiting hairless protein  
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
CC human hairless protein mRNA immediately after nucleotide 2033.  
CC  
XX  
SQ Sequence 29 BP; 7 A; 5 C; 13 G; 4 T; 0 other;  
Query Match 92.5%; Score 14.8; DB 25; Length 29;  
Best Local Similarity 87.5%; Pred. No. 93;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGGCTAGCHACACGA 16  
Db 7 GGGCTAGCTACACGA 22  
RESULT 35  
ID ABX13998  
AC ABX13998 standard; DNA; 29 BP.  
XX  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2047.  
XX  
XX Catalytic DNA; catalytic RNA; hairless protein; ss;  
KM hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;  
KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KM catalytic core; cleavage site; pharmaceutical; hair production;  
KM hair follicle; anagen phase; catagen phase; hair removal product;  
KM depilatory.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH 8..22  
FT misc\_feature /tag= a  
FT /note= "Catalytic domain"  
XX  
XX WO200283891-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 12-APR-2002; 2002WO-US11683.  
XX  
XX 13-APR-2001; 2001US-283618P.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX Christiano AM;  
XX  
XX WPI; 2003-093020/08.  
XX  
XX  
XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
XX Protein mRNA, useful for inhibiting hair production by a hair-producing  
XX cell, or for inhibiting transition of a hair follicle from anagen phase  
XX to catagen phase -  
XX  
XX Claim 3; Page 35; 65pp; English.  
XX  
XX The invention discloses a new catalytic DNA or RNA molecule that

CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
CC which comprises a catalytic domain that cleaves mRNA at a defined  
CC consensus sequence and binding domain contiguous with the 5' and 3' ends  
CC of the catalytic domain. Lack of expression of the hairless gene due to  
CC inherited mutations leads to the complete loss of hair, known as  
CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
CC the genes promoting hair growth, and one way to get targeted, transient  
CC gene suppression is through the use of catalytic nucleic acid technology,  
CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
CC a self-catalytic enzymatic function and sequence specific RNA binding  
CC ability. Small DNA oligonucleotides that have a similar structure to the  
CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
CC more lenient consensus cleavage site requirements and are less likely to  
CC degrade, *in vivo*, than hammerhead ribozymes. The catalytic nucleic acids  
CC are useful in pharmaceutical compositions for inhibiting hair production  
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
CC the transition of a hair follicle from the anagen phase to the catagen  
CC phase. A non-human transgenic mammal is useful as a model for testing  
CC hair removal products which function by inhibiting hairless protein  
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
CC human hairless protein mRNA immediately after nucleotide 2047.

SQ Sequence 29 BP; 9 A; 10 C; 7 G; 3 T; 0 other;

Query Match	92.5%	Score 14.8	DB 25	Length 29
Best Local Similarity	87.5%	Pred. No. 93		
Best Match 14; Conservative	2	Mismatches 0	Indels 0	Gaps 0

OY	1	RGCTAGCHACACGA	16
		:     :	
Db	7	GGCTAGCTACACGA	22

Db 7 GGGCTAGCTACACGA 22

RESULT 36  
ABX13999  
ID ABX13999 standard; DNA; 29 BP.

DT	25-FEB-2003 (first entry)
XX	
DE	Deoxy-ribosome, cleaving hairless protein mRNA after nucleotide 2083

KW Catalytic DNA; catalytic RNA; hairless protein; ss;  
KW hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;  
KW ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme  
KW catalytic core; cleavage site; pharmaceutical; hair production;  
KW hair follicle; anagen phase; catagen phase; hair removal product;  
KW depilatory.

OS	Homo sapiens.
OS	Synthetic.

Synthetic

	Location/Qualifiers
FH Key	8..22
FT misc_feature	/*tag= a
FT	/note= "Catalytic domain"
FT	

PN WO200283891-A2

PD 24-OCT-2002

PF 12-APR-2002; 2002WO-US11683.

PR 13-APR-2001; 2001US-283618P.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Christiano AM;

DR WPI; 2003-093020/08

PR New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PR protein mRNA, useful for inhibiting hair production by a hair-producing  
 PR cell, or for inhibiting transition of a hair follicle from anagen phase  
 PR to catagen phase -  
 XX  
 PS Claim 3, Page 35, 65pp, English.

PS Claim 3; Page 35; 65pp; English.

CC The invention discloses a new catalytic DNA or RNA molecule that  
CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
CC which comprises a catalytic domain that cleaves mRNA at a defined  
CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
CC of the catalytic domain. Lack of expression of the hairless gene due to  
CC inherited mutations leads to the complete loss of hair. Known as  
CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
CC the genes promoting hair growth, and one way to get targeted, transient  
CC gene suppression is through the use of catalytic nucleic acid technology,  
CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
CC a self-catalytic enzymatic function and sequence specific RNA binding  
CC ability. Small DNA oligonucleotides that have a similar structure to the  
CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
CC more lenient consensus cleavage site requirements and are less likely to  
CC degrade, *in vivo*, than hammerhead ribozymes. The catalytic nucleic acids  
CC are useful in pharmaceutical compositions for inhibiting hair production  
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
CC the transition of a hair follicle from the anagen phase to the catagen  
CC phase. A non-human transgenic mammal is useful as a model for testing  
CC hair removal products which function by inhibiting hairless protein  
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
CC human hairless protein mRNA immediately after nucleotide 2083.

Sequence 29 BP; 9 A; 7 C; 9 G; 4 T; 0 other;

Query Match	92.5%	Score 14.8	DB 25	Length 29
Best Local Similarity	87.5%	Pred. No. 93		
Matches 14; Conservative	2	Mismatches	0	Indels 0; Gaps 0.

```

QY      1 RGCCTAGCHACACGA 16
          :|||||:|||||
Db      7 GGCCTAGCTACACGA 22

```

Db 7 GGGCTAGCTACCAACGA 22

RESULT 37  
ABX14001  
ID ABX14001 standard; DNA; 29 BP.

DT	25-FEB-2003 (first entry)
XX	
DE	Deoxy-ribosyme, cleaving hairless protein mRNA after nucleotide 2380

KM Catalytic DNA; catalytic RNA; hairless protein; ss;  
KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
KM ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KM catalytic core; cleavage site; pharmaceutical; hair production;  
KM hair follicle; anagen phase; catagen phase; hair removal product;  
KM depilatory.

OS	Homo sapiens
OS	Synthetic.

OS Synthetic

	Key	Location/Qualifiers
FH	misc_feature	8..22
FT		/*tag= a
FT		/note= "Catalytic domain"

PN WO200283891-A2

PD 24-OCT-2002

PF 12-APR-2002; 2002WO-US11683.

PR 13-APR-2001; 2001US-283618P.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX  
 XX  
 PI Cristiano AM;  
 XX  
 DR WPI: 2003-093020/08.  
 XX  
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase  
 XX  
 PS Claim 3; Page 35; 65pp; English.  
 CC The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 2380.  
 XX  
 XX Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;  
 SQ  
 QY Query Match 92.5%; Score 14.8; DB 25; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 RGGCTAGCHCAACGA 16  
 :|||||:|||||  
 7 AGGCTAGCTACACGA 22  
 RESULT 38  
 ABX14002 standard; DNA; 29 BP.  
 ID ABX14002 standard; DNA; 29 BP.  
 AC  
 XX ABX14002;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2395.  
 XX  
 XX Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
 KW ribozyme; DNAzyme; self-catalytic; hammerhead; deoxy-ribozyme;  
 KW catalytic core; cleavage site; pharmaceutical; hair production;  
 KW hair follicle; anagen phase; catagen phase; hair removal product;  
 KW depilatory.  
 KW  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 8..22  
 FT /\*tag= a

FT /note= "Catalytic domain"  
 XX  
 XX WO200283891-A2.  
 XX  
 XX PD 24-OCT-2002.  
 XX  
 XX PF 12-APR-2002; 2002WO-US11683.  
 XX  
 XX PR 13-APR-2001; 2001US-283618P.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX  
 XX Cristiano AM;  
 PI  
 XX WPI: 2003-093020/08.  
 DR  
 XX  
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase  
 XX  
 PS Claim 3; Page 35; 65pp; English.  
 CC The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 2395.  
 XX  
 XX Sequence 29 BP; 9 A; 9 C; 8 G; 3 T; 0 other;  
 SQ  
 QY Query Match 92.5%; Score 14.8; DB 25; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 RGGCTAGCHCAACGA 16  
 :|||||:|||||  
 7 GGGCTAGCTACACGA 22  
 RESULT 39  
 AAA14525/c  
 ID AAA14525 standard; DNA; 30 BP.  
 XX  
 XX AAA14525;  
 AC  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Oligonucleotide 5'-polynm-gaglink-(pleio)-DNase-1023-B/P.  
 XX  
 XX Reverse transcriptase; RNase H; stem-loop structure; genetic element;  
 KW inverted tandem repeat; vector; inhibitory nucleic acid;  
 KW antisense sequence; aptamer; gene expression; ss.  
 XX  
 OS Synthetic.

XX PN WO200022114-A1.  
 XX XX 20-APR-2000.  
 XX PF 12-OCT-1999; 99WO-US23936.  
 XX PR 09-OCT-1998; 98US-0169793.  
 PR 16-SEP-1999; 99US-0397782.  
 PR 04-OCT-1999; 99US-0169793.  
 XX (INGE-) INGENE INC.  
 XX Conrad CA;  
 PI WPI; 2000-317974/27.  
 XX Genetic element for producing and delivering single-stranded DNA,  
 PT comprises a gene encoding reverse transcriptase and a sequence of  
 PT interest flanked by an inverted tandem repeat and primer binding site  
 PT  
 PS Disclosure; Page 45; 77pp; English.  
 XX The specification describes methods for producing single-stranded cDNA  
 CC (sscDNA) in eukaryotic cells. They use a DNA cassette that produces  
 CC sscDNA in vivo. The cassette contains the Moloney murine leukemia virus  
 CC reverse transcriptase/RNase H, a bacterial restriction endonuclease  
 CC gene, and a sequence of interest which produces a RNA template from  
 CC which the reverse transcriptase synthesizes cDNA of a specified sequence.  
 CC The sscDNA is then modified to remove all flanking vector sequences by  
 CC taking advantage of the stem-loop structure of the cDNA, which forms as  
 CC a result of the inclusion of an inverted tandem repeat that allows the  
 CC sscDNA to fold back on itself, forming a double stranded DNA stem, in  
 CC the sequence of interest. The double-stranded stem contains one or more  
 CC functional genetic elements (GE), adapted for incorporation into a vector  
 CC for delivery to a cell. The vectors are is useful for producing a sscDNA  
 CC sequence of interest, particularly a cDNA transcript, an inhibitory  
 CC nucleic acid molecule which is an antisense sequence or aptamer, an mRNA  
 CC transcript and a heteroduplex molecule. Inhibitory nucleic acid molecules  
 CC to a target cell are useful for alleviating pathological conditions by  
 CC regulating gene expression. The present oligonucleotide was used to  
 CC produce a vector for use in the course of the invention.  
 XX  
 SQ Sequence 30 BP; 5 A; 8 C; 8 G; 9 T; 0 other;  
 Query Match 92.5%; Score 14.8; DB 21; Length 30;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGCTAGCHACACGA 16  
 :|||||:|||||  
 Db 24 AGGCTAGCTACACGA 9  
 RESULT 40  
 AA287648 ID AA287648 standard; DNA; 30 BP.  
 XX AC AA287648;  
 XX 09-MAY-2000 (first entry)  
 DE Human short protein kinase C (PKC)alpha DNA ribozyme.  
 XX Ribozyme; hammerhead: RNAase degradation; catalytic; PKCalpha; VEGF;  
 KM protein kinase C alpha; tumour necrosis factor alpha; TNFalpha; cancer;  
 KM vascular epithelial growth factor; gene expression; malignant glioma;  
 XX cell proliferation; cytostatic; human; ss.  
 OS Homo sapiens.  
 XX WO9963066-A2.  
 PN

XX PD 09-DEC-1999.  
 XX PF 28-MAY-1999; 99WO-GB01706.  
 XX PR 01-JUN-1998; 98GB-0011750.  
 XX (NOR-) NORWEGIAN RADTUM HOSPITAL RES FOUND.  
 PA (DZIE/) DZIEGLAWSKA H E.  
 XX Sloud M;  
 PI WPI; 2000-147046/13.  
 DR Novel ribozymes, used for inhibiting the proliferation of cells, e.g.  
 XX for treating or preventing cancers  
 PT  
 PS Disclosure; Page 9; 93pp; English.  
 XX The invention provides novel modified ribozymes that have 3 or more  
 CC pyrimidine nucleotides (PMN) in the ribozyme modified at the 2'-position,  
 CC where the PMNs are modified to 2'-amino PMNs and the ribozymes exhibit  
 CC improved stability to RNAase degradation and exhibits 85% or more  
 CC catalytic activity of the unmodified ribozymes. The ribozymes of the  
 CC invention are selected from rat and human protein kinase C (PKC)alpha  
 CC ribozymes, tumour necrosis factor (TNF)alpha ribozyme, rat and human  
 CC vascular epithelial growth factor (VEGF) ribozymes. These ribozymes can  
 CC be used for treating or preventing a disease or condition responsive to  
 CC an alteration in the expression of a gene, where the ribozyme is capable  
 CC of cleaving the RNA transcribed from the gene. They can be used for  
 CC treating or preventing a disease or condition associated with the  
 CC proliferation of rapidly dividing cells, e.g. cancer such as malignant  
 CC glioma. They can also be used for inhibiting the proliferation of cells.  
 CC The use of 2'-amino modified pyrimidine can provide ribozymes of improved  
 CC stability which retain the activity of the unmodified ribozyme. The  
 CC present sequence represents a human short PKCalpha DNA ribozyme.  
 XX  
 SQ Sequence 30 BP; 7 A; 11 C; 8 G; 4 T; 0 other;  
 Query Match 92.5%; Score 14.8; DB 21; Length 30;  
 Best Local Similarity 87.5%; Pred. No. 93;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGCTAGCHACACGA 16  
 :|||||:|||||  
 Db 8 AGGCTAGCTACACGA 23  
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 Job time : 153.5 secs

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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 05:19:13 ; Search time 1004.5 Seconds

(without alignments)  
651.622 Million cell updates/sec

Title: US-09-423-035B-122

Perfect score: 16

Sequence: 1 rgcctagchacaaga 16

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1520254

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 1000 summaries

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2: gb_hcg: *
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6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vt: *
15: gb_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
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20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vt: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	14.8	92.5	16	6	AX274735 Sequence
5	14.8	92.5	16	6	AX282449 Sequence
6	14.8	92.5	16	6	AX427010 Sequence
7	14.8	92.5	16	6	AX583609 Sequence
8	14.8	92.5	29	6	AR201808 Sequence
9	14.8	92.5	29	6	AR201810 Sequence
10	14.8	92.5	30	6	AR201840 Sequence
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18	14.8	92.5	31	6	AR116975 Sequence
19	14.8	92.5	31	6	AR201827 Sequence
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21	14.8	92.5	31	6	AR201833 Sequence
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230	14.8	92.5	31	6	AX220752	Sequence	303	14.8	92.5	31	6	AX220825	Sequence	AX220825
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234	14.8	92.5	31	6	AX220756	Sequence	307	14.8	92.5	31	6	AX220829	Sequence	AX220829
235	14.8	92.5	31	6	AX220757	Sequence	308	14.8	92.5	31	6	AX220830	Sequence	AX220830
236	14.8	92.5	31	6	AX220758	Sequence	309	14.8	92.5	31	6	AX220831	Sequence	AX220831
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 ORGANISM synthetic construct

REFERENCE 1 artificial sequences.  
 AUTHORS Krupp, G.  
 JOURNAL Patent: DE 19915141-A 4 28-SEP-2000;  
 ARTUS GES FUER MOLEKULARBIOLOG (DE)  
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 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Blatt, L., Meswigen, J. and Chowrira, B.M.  
 TITLE Method and reagent for the modulation and diagnosis of cdk20 and  
 nogo gene expression  
 JOURNAL Patent: WO 0159103-A 9268 16-AUG-2001;  
 RHOZOME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
 McSwiggen, James (US); Chowrira, Bharat M. (US)  
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 VERSION AX229619.1 GI:15558760  
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 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 REFERENCE 1  
 AUTHORS Fattaey, A.R., Jarvis, T., Meswigen, J., Bochner, R.N. and Holman, P.S.  
 TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk  
 1) enzyme  
 JOURNAL Patent: WO 0157206-A 2991 09-AUG-2001;

FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; Fatarey, Ali R. (US)  
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ACCESSION AX274735  
VERSION AX274735.1 GI:16547474  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 2304 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
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ACCESSION AX282449  
VERSION AX282449.1 GI:16609580  
KEYWORDS  
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ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Uman,N., Mcswiggen,J.A., Zinnen,S., Seiwert,S., Haeblerl,P., Chowrira,B. and Blatt,L.  
TITLE Nucleic acid sensor molecules  
JOURNAL Patent: WO 0166721-A 21 13-SEP-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US)  
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DEFINITION Sequence 5346 from Patent WO0188124.  
ACCESSION AX427010  
VERSION AX427010.1 GI:2150396  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswiggen,J.A., McLaughlin,P.G. and Randi,A.M.  
TITLE Method and reagent for the inhibition of erg  
JOURNAL Patent: WO 0188124-A 5346 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
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LOCUS AX583609 16 bp DNA linear PAT 10-JAN-2003  
DEFINITION Sequence 5447 from Patent WO0211674.  
ACCESSION AX583609  
VERSION AX583609.1 GI:27655419  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1)  
JOURNAL Patent: WO 0211674-A 5447 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)  
FEATURES  
SOURCE 1. .16  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

Query Match 92.5%; Score 14.8; DB 6; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 3.1e+02;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16  
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 Db 1 RGGCTAGCTACAACGA 16

RESULT 8  
 AR201808 29 bp DNA linear PAT 20-APR-2002  
 LOCUS AR201808  
 DEFINITION Sequence 23 from patent US 6361941.  
 ACCESSION AR201808  
 VERSION AR201808.1 GI:20256347  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 1 (bases 1 to 29)  
 AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
 TITLE Catalytic nucleic acid-based diagnostic methods  
 JOURNAL Patent: US 6361941-A 23 26-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..29  
 /organism="unknown"

BASE COUNT 10 a 5 c 10 g 3 t 1 others

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16  
 :|||||:|||||  
 Db 8 AGGCTAGCTACAACGA 23

RESULT 9  
 AR201810 29 bp DNA linear PAT 20-APR-2002  
 LOCUS AR201810  
 DEFINITION Sequence 25 from patent US 6361941.  
 ACCESSION AR201810  
 VERSION AR201810.1 GI:20256349  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 1 (bases 1 to 29)  
 AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
 TITLE Catalytic nucleic acid-based diagnostic methods  
 JOURNAL Patent: US 6361941-A 25 26-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..29  
 /organism="unknown"

BASE COUNT 7 a 10 c 5 g 7 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 29;  
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16  
 :|||||:|||||  
 Db 9 AGGCTAGCTACAACGA 24

RESULT 10  
 AR201840 30 bp DNA linear PAT 20-APR-2002  
 LOCUS AR201840  
 DEFINITION Sequence 55 from patent US 6361941.  
 ACCESSION AR201840

VERSION AR201840.1 GI:20256379  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 1 (bases 1 to 30)  
 AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
 TITLE Catalytic nucleic acid-based diagnostic methods  
 JOURNAL Patent: US 6361941-A 55 26-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..30  
 /organism="unknown"

BASE COUNT 12 a 7 c 5 g 6 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;  
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16  
 :|||||:|||||  
 Db 8 AGGCTAGCTACAACGA 23

RESULT 11  
 AX009377 30 bp DNA linear PAT 06-SEP-2000  
 LOCUS AX009377  
 DEFINITION Sequence 7 from Patent WO9963066.  
 ACCESSION AX009377  
 VERSION AX009377.1 GI:9996678  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE  
 1  
 AUTHORS Sloud,M.  
 TITLE Amino-modified ribozymes  
 JOURNAL Patent: WO 9963066-A 7 09-DEC-1999;  
 DZIEGLEWSKA HANNA EVA (GB); STODD MOUNUDY (NO); NORWEGIAN RADTUM HOSPITAL RESE (NO)  
 FEATURES Location/Qualifiers  
 source 1..30  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="PKC alpha ribozyme"

BASE COUNT 7 a 11 c 8 g 4 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;  
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16  
 :|||||:|||||  
 Db 8 AGGCTAGCTACAACGA 23

RESULT 12  
 AX111628 30 bp DNA linear PAT 30-APR-2001  
 LOCUS AX111628/c  
 DEFINITION Sequence 3 from Patent WO0125419.  
 ACCESSION AX111628  
 VERSION AX111628.1 GI:13927904  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE  
 1  
 AUTHORS Conrad,C.A. and Chen,Y.  
 TITLE Altering gene expression with ssdna produced in vivo  
 JOURNAL Patent: WO 0125419-A 3 12-APR-2001;  
 Cytogenix, Inc. (US)

FEATURES  
source  
1. 30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide"

BASE COUNT 5 a 8 c 8 g 9 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
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24 AGGCTAGCTACACGA 9

Db

RESULT 13  
LOCUS AX274718 30 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 2287 from Patent WO0162911.  
ACCESSION AX274718  
VERSION AX274718.1 GI:16547457  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., Hamblin,P.A. and Ellis,J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNML Patent: WO 0162911-A 2287 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
FEATURES  
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1. 30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
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/note="2'-O-Methyl"  
misc\_feature 23. .29  
/note="2'-O-Methyl"  
misc\_feature 30  
/note="n stands for inverted deoxyabasic derivative"  
BASE COUNT 7 a 9 c 6 g 7 t 1 others  
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
7 GGGCTAGCTACACGA 22

Db

RESULT 14  
LOCUS AX274719 30 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 2288 from Patent WO0162911.  
ACCESSION AX274719  
VERSION AX274719.1 GI:16547458  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., Hamblin,P.A. and Ellis,J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNML Patent: WO 0162911-A 2288 30-AUG-2001;

FEATURES  
source  
1. 30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

BASE COUNT 10 a 7 c 7 g 5 t 1 others

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
7 AGGCTAGCTACACGA 22

Db

RESULT 15  
LOCUS AX274720 30 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 2289 from Patent WO0162911.  
ACCESSION AX274720  
VERSION AX274720.1 GI:16547459  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., Hamblin,P.A. and Ellis,J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNML Patent: WO 0162911-A 2289 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
FEATURES  
source  
1. 30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
misc\_feature 1. .7  
/note="2'-O-Methyl"  
misc\_feature 23. .29  
/note="2'-O-Methyl"  
misc\_feature 30  
/note="n stands for inverted deoxyabasic derivative"  
BASE COUNT 10 a 4 c 9 g 6 t 1 others  
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16  
:|||||:|||||  
7 AGGCTAGCTACACGA 22

Db

RESULT 16  
LOCUS AX274721 30 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 2290 from Patent WO0162911.  
ACCESSION AX274721  
VERSION AX274721.1 GI:16547460  
KEYWORDS  
SOURCE synthetic construct

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ORGANISM    synthetic construct
REFERENCE    artificial sequences.
AUTHORS      1 Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and
              Ellis, J.H.
TITLE        Method and reagent for the inhibition of grid
JOURNAL      Patent: WO 0162911-A 2290 30-AUG-2001; GLAXO GROUP LIMITED (GB)
FEATURES     RIBOZYME PHARMACEUTICALS, INC. (US)
SOURCE       location/Qualifiers
1. 30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
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/note="2'-O-Methyl"
misc_feature 23. 29
/note="2'-O-Methyl"
misc_feature 30
/note="n strands for inverted deoxyabasic derivative"
BASE COUNT 9 a 4 c 10 g 6 t 1 others
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
Db 7 AGGCTAGCTACACGA 22

RESULT 17
LOCUS      AX274722 30 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 2291 from Patent WO0162911.
ACCESSION  AX274722
VERSION     AX274722.1 GI:16547461
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE    1 Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and
              Ellis, J.H.
TITLE        Method and reagent for the inhibition of grid
JOURNAL      Patent: WO 0162911-A 2291 30-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES     location/Qualifiers
1. 30
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/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
misc_feature 1. 7
/note="2'-O-Methyl"
misc_feature 23. 29
/note="2'-O-Methyl"
misc_feature 30
/note="n strands for inverted deoxyabasic derivative"
BASE COUNT 8 a 7 c 10 g 4 t 1 others
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
Db 7 GGGCTAGCTACACGA 22

RESULT 18

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AR116975    AR116975 31 bp DNA linear PAT 16-MAY-2001
LOCUS      Sequence 5 from patent US 6140055.
DEFINITION AR116975
ACCESSION  AR116975
VERSION     AR116975.1 GI:14097881
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 31)
AUTHORS      Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE        Zymogenic nucleic acid detection methods and related kits
JOURNAL      Patent: US 6140055-A 5 31-OCT-2000;
              Location/Qualifiers
1. 31
/organism="unknown"
BASE COUNT 10 a 7 c 7 g 7 t
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
Db 8 AGGCTAGCTACACGA 23

RESULT 19
LOCUS      AR201827 31 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 42 from patent US 6361941.
ACCESSION  AR201827
VERSION     AR201827.1 GI:20256366
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 31)
AUTHORS      Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE        Catalytic nucleic acid-based diagnostic methods
JOURNAL      Patent: US 6361941-A 42 26-MAR-2002;
              Location/Qualifiers
1. 31
/organism="unknown"
BASE COUNT 10 a 10 c 5 g 6 t
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
Db 10 AGGCTAGCTACACGA 25

RESULT 20
LOCUS      AR201830 31 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 45 from patent US 6361941.
ACCESSION  AR201830
VERSION     AR201830.1 GI:20256369
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 31)
AUTHORS      Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE        Catalytic nucleic acid-based diagnostic methods
JOURNAL      Patent: US 6361941-A 45 26-MAR-2002;
              Location/Qualifiers
1. 31

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BASE COUNT 11 a 9 c 5 g 6 t  
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16  
Db 10 AGGCTAGCTACAAGA 25

RESULT 21  
LOCUS AR201833 31 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 48 from patent US 6361941.  
ACCESSION AR201833  
VERSION AR201833.1 GI:20256372  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)  
AUTHORS Todd A.V., Puery,C.J. and Cairns,M.J.  
TITLE Catalytic nucleic acid-based diagnostic methods  
JOURNAL Patent: US 6361941-A 48 26-MAR-2002;  
FEATURES Location/Qualifiers  
source 1. .31

BASE COUNT 10 a 6 c 12 g 3 t  
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16  
Db 9 GGGCTAGCTACAAGA 24

RESULT 22  
LOCUS AR201836 31 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 51 from patent US 6361941.  
ACCESSION AR201836  
VERSION AR201836.1 GI:20256375  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)  
AUTHORS Todd A.V., Puery,C.J. and Cairns,M.J.  
TITLE Catalytic nucleic acid-based diagnostic methods  
JOURNAL Patent: US 6361941-A 51 26-MAR-2002;  
FEATURES Location/Qualifiers  
source 1. .31

BASE COUNT 11 a 6 c 11 g 3 t  
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16  
Db 9 AGGCTAGCTACAAGA 24

RESULT 23  
AR204371

LOCUS AR204371 31 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 5 from patent US 6365724.  
ACCESSION AR204371  
VERSION AR204371.1 GI:21501005  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)  
AUTHORS Todd A.V., Puery,C.J. and Cairns,M.J.  
TITLE Zymogenic nucleic acid detection methods, and related molecules and kits  
JOURNAL Patent: US 6365724-A 5 02-APR-2002;  
FEATURES Location/Qualifiers  
source 1. .31

BASE COUNT 10 a 7 c 7 g 7 t  
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16  
Db 8 AGGCTAGCTACAAGA 23

RESULT 24  
LOCUS AX220546 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5988 from Patent W00159103.  
ACCESSION AX220546  
VERSION AX220546.1 GI:15548270  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1  
AUTHORS Blatt,L., Meswigen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5988 16-AUG-2001;  
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; Meswigen, James (US) ; Chowrira, Bharat M. (US)  
source 1. .31

FEATURES  
source 1. .31  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 10 a 8 c 8 g 5 t  
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16  
Db 8 GGGCTAGCTACAAGA 23

RESULT 25  
LOCUS AX220547 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5989 from Patent W00159103.  
ACCESSION AX220547  
VERSION AX220547.1 GI:15548271  
KEYWORDS

SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 5989 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
source 1.31  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 10 a 7 c 11 g 3 t

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACA 16  
8 GGGCTAGCTACAACA 23

RESULT 26  
AX220548 31 bp DNA linear PAT 07-SEP-2001  
LOCUS Sequence 5990 from Patent WO0159103.  
DEFINITION AX220548  
ACCESSION AX220548.1 GI:15548272  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5990 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
source 1.31  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 9 a 8 c 6 g 8 t

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACA 16  
8 AGGCTAGCTACAACA 23

RESULT 27  
AX220549 31 bp DNA linear PAT 07-SEP-2001  
LOCUS Sequence 5991 from Patent WO0159103.  
DEFINITION AX220549  
ACCESSION AX220549.1 GI:15548273  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL nogo gene expression  
Patent: WO 0159103-A 5991 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
source 1.31  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 11 a 7 c 8 g 5 t

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACA 16  
8 AGGCTAGCTACAACA 23

RESULT 28  
AX220550 31 bp DNA linear PAT 07-SEP-2001  
LOCUS Sequence 5992 from Patent WO0159103.  
DEFINITION AX220550  
ACCESSION AX220550.1 GI:15548274  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5992 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
source 1.31  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 10 a 7 c 7 g 7 t

Query Match 92.5%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACA 16  
8 GGGCTAGCTACAACA 23

RESULT 29  
AX220551 31 bp DNA linear PAT 07-SEP-2001  
LOCUS Sequence 5993 from Patent WO0159103.  
DEFINITION AX220551  
ACCESSION AX220551.1 GI:15548275  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5993 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

FEATURES  
source  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
1. .31  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT  
ORIGIN  
9 a 5 c 10 g 7 t

Query Match  
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RESULT 30  
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LOCUS  
DEFINITION  
Sequence 5994 from Patent WO0159103.  
ACCESSION  
AX220552  
VERSION  
AX220552.1 GI:15548276  
KEYWORDS  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

REFERENCE  
1  
AUTHORS  
Blatt, L., McSwiggen, J. and Chowrira, B. M.  
TITLE  
Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL  
Patent: WO 0159103-A 5994 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
location/Qualifiers

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Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  
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RESULT 31  
AX220553 31 bp DNA linear PAT 07-SEP-2001  
LOCUS  
DEFINITION  
Sequence 5995 from Patent WO0159103.  
ACCESSION  
AX220553  
VERSION  
AX220553.1 GI:15548277  
KEYWORDS  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

REFERENCE  
1  
AUTHORS  
Blatt, L., McSwiggen, J. and Chowrira, B. M.  
TITLE  
Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL  
Patent: WO 0159103-A 5995 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
location/Qualifiers

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RESULT 32  
AX220554 31 bp DNA linear PAT 07-SEP-2001  
LOCUS  
DEFINITION  
Sequence 5996 from Patent WO0159103.  
ACCESSION  
AX220554  
VERSION  
AX220554.1 GI:15548278  
KEYWORDS  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

REFERENCE  
1  
AUTHORS  
Blatt, L., McSwiggen, J. and Chowrira, B. M.  
TITLE  
Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL  
Patent: WO 0159103-A 5996 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
location/Qualifiers

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ACCESSION  
AX220555  
VERSION  
AX220555.1 GI:15548279  
KEYWORDS  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

REFERENCE  
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AUTHORS  
Blatt, L., McSwiggen, J. and Chowrira, B. M.  
TITLE  
Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL  
Patent: WO 0159103-A 5997 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
location/Qualifiers

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Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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8 GGGCTAGCTACACGA 23

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LOCUS Sequence 5998 from Patent WO0159103.  
DEFINITION AX220556  
ACCESSION AX220556.1 GI:15548280  
VERSION  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.  
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and  
TITLE nogo gene expression  
JOURNAL Patent: WO 0159103-A 5998 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

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Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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8 GGGCTAGCTACACGA 23

RESULT 35  
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LOCUS Sequence 5999 from Patent WO0159103.  
DEFINITION AX220557  
ACCESSION AX220557.1 GI:15548281  
VERSION  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.  
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and  
TITLE nogo gene expression  
JOURNAL Patent: WO 0159103-A 5999 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

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Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 6000 from Patent WO0159103.  
DEFINITION AX220558  
ACCESSION AX220558.1 GI:15548282  
VERSION  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.  
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and  
TITLE nogo gene expression  
JOURNAL Patent: WO 0159103-A 6000 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

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8 AGGCTAGCTACACGA 23

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AX220559 31 bp DNA linear PAT 07-SEP-2001  
LOCUS Sequence 6001 from Patent WO0159103.  
DEFINITION AX220559  
ACCESSION AX220559.1 GI:15548283  
VERSION  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.  
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and  
TITLE nogo gene expression  
JOURNAL Patent: WO 0159103-A 6001 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

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Query Match 92.5%; Score 14.8; DB 6; Length 31;  
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DEFINITION Sequence 6002 from Patent WO0159103.  
ACCESSION AX220560  
VERSION AX220560.1 GI:15548284  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS Blatt, L., McSwiggen, J. and Chowitra, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
JOURNAL nogo gene expression  
PATENT: WO 0159103-A 6002 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowitra, Bharat M. (US)  
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Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 8 AGGCTAGCTACACGA 23

RESULT 39  
AX220561  
LOCUS AX220561 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 6003 from Patent WO0159103.  
ACCESSION AX220561  
VERSION AX220561.1 GI:15548285  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS Blatt, L., McSwiggen, J. and Chowitra, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
JOURNAL nogo gene expression  
PATENT: WO 0159103-A 6003 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowitra, Bharat M. (US)  
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Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 40  
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LOCUS AX220562 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 6004 from Patent WO0159103.  
ACCESSION AX220562  
VERSION AX220562.1 GI:15548286  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS Blatt, L., McSwiggen, J. and Chowitra, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
JOURNAL nogo gene expression  
PATENT: WO 0159103-A 6004 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowitra, Bharat M. (US)  
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BASE COUNT 13 a 6 c 7 g 5 t  
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Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16  
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Db 8 GGGCTAGCTACACGA 23

Search completed: January 21, 2004, 07:26:45  
Job time : 1007 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 05:19:13 ; Search time 1004.5 Seconds

(without alignments)  
651.622 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16

Sequence: 1 rgctagctacacga 16

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1520254

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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and is derived by analysis of the total score distribution.

## SUMMARIES

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artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., Mcswigen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
JOURNAL nogo gene expression  
Patent: WO 0159103-A 9268 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
Mcswigen, James (US) ; Chowrira, Bharat M. (US)  
Location/Qualifiers

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SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and  
Ellis, J.H.  
TITLE Method and reagent for the inhibition of grid

artificial sequences.

REFERENCE 1  
AUTHORS Fattaey, A.R., Jarvis, T., Mcswigen, J., Bocher, R.N. and Holman, P.S.  
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk  
1) enzyme  
Patent: WO 0157206-A 2991 09-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)  
Location/Qualifiers

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JOURNAL Patent: WO 0162911-A 2304 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

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artificial sequences.

REFERENCE 1  
AUTHORS Ueman,N., Mcswigen,J.A., Zinnen,S., Seiwert,S., Haeblerl,P.,  
Chowrira,B. and Blatl,J.  
TITLE Nucleic acid sensor molecules  
JOURNAL Patent: WO 0166721-A 21 13-SEP-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US)  
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ACCESSION AX427010  
VERSION AX427010.1 GI:21530396  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Jarvis,T., von Carlowitz,I., Mcswigen,J.A., McLaughlin,F.G. and  
Randi,A.M.  
TITLE Method and reagent for the inhibition of erg  
JOURNAL Patent: WO 0188124-A 5346 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
FEATURES  
SOURCE  
1. .16  
/organism="synthetic construct"

/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

BASE COUNT 5 a 4 c 4 g 2 t 1 others

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
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1 RGGCTAGCTACACGA 16

RESULT 6  
AX583609 16 bp DNA linear PAT 10-JAN-2003  
LOCUS  
DEFINITION Sequence 5447 from Patent WO0211674.  
ACCESSION AX583609  
VERSION AX583609.1 GI:27655419  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.  
and Grupe,A.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
JOURNAL Patent: WO 0211674-A 5447 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
FEATURES  
SOURCE  
1. .16  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

BASE COUNT 5 a 4 c 4 g 2 t 1 others

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
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1 RGGCTAGCTACACGA 16

RESULT 7  
AR201808 29 bp DNA linear PAT 20-APR-2002  
LOCUS  
DEFINITION Sequence 23 from patent US 6361941.  
ACCESSION AR201808  
VERSION AR201808.1 GI:20256347  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 29)  
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
TITLE Catalytic nucleic acid-based diagnostic methods  
JOURNAL Patent: US 6361941-A 23 26-MAR-2002;  
FEATURES  
SOURCE  
1. .29  
/organism="unknown"

BASE COUNT 10 a 5 c 10 g 3 t 1 others

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 29;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
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8 AGGCTAGCTACACGA 23

RESULT 8  
AR201810 29 bp DNA linear PAT 20-APR-2002

LOCUS AR201810  
DEFINITION Sequence 25 from patent US 6361941.  
ACCESSION AR201810  
VERSION AR201810.1 GI:20256349

KEYWORDS  
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 29)  
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
TITLE Catalytic nucleic acid-based diagnostic methods  
JOURNAL Patent: US 6361941-A 25 26-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..29  
/organism="unknown"

BASE COUNT 7 a 10 c 5 g 7 t  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 29;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
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9 AGGCTAGCTACACGA 24

Db

RESULT 9  
AR201840 30 bp DNA linear PAT 20-APR-2002

LOCUS AR201840  
DEFINITION Sequence 55 from patent US 6361941.  
ACCESSION AR201840  
VERSION AR201840.1 GI:20256379

KEYWORDS  
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)  
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
TITLE Catalytic nucleic acid-based diagnostic methods  
JOURNAL Patent: US 6361941-A 55 26-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"

BASE COUNT 12 a 7 c 5 g 6 t  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;  
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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
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8 AGGCTAGCTACACGA 23

Db

RESULT 10  
AX009377 30 bp DNA linear PAT 06-SEP-2000

LOCUS AX009377  
DEFINITION Sequence 7 from Patent WO9963066.  
ACCESSION AX009377  
VERSION AX009377.1 GI:9996678  
KEYWORDS  
SOURCE synthetic construct

ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Stoud,M.  
TITLE Amino-modified ribozymes  
JOURNAL Patent: WO 9963066-A 7 09-DEC-1999;  
DZIEGLESKA HANNA EVA (GB); STOUD MOULDY (NO); NORWEGIAN RADIIUM  
HOSPITAL RESE (NO)

FEATURES Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="PKC alpha ribozyme"

BASE COUNT 7 a 11 c 8 g 4 t  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
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8 AGGCTAGCTACACGA 23

Db

RESULT 11  
AX111628 30 bp DNA linear PAT 30-APR-2001

LOCUS AX111628  
DEFINITION Sequence 3 from Patent WO0125419.  
ACCESSION AX111628  
VERSION AX111628.1 GI:13927904

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1

AUTHORS Conrad,C.A. and Chen,Y.  
TITLE Altering gene expression with adna produced in vivo  
JOURNAL Patent: WO 0125419-A 3 12-APR-2001;  
Cyrogenix, Inc. (US)

FEATURES Location/Qualifiers  
source 1..30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide"

BASE COUNT 5 a 8 c 8 g 9 t  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
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24 AGGCTAGCTACACGA 9

Db

RESULT 12  
AX274718 30 bp DNA linear PAT 29-OCT-2001

LOCUS AX274718  
DEFINITION Sequence 2287 from Patent WO0162911.  
ACCESSION AX274718  
VERSION AX274718.1 GI:16547457

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Garvis,T., von Carlwiltz,I., Mcswigen,J.A., Hamblin,P.A. and  
Ellis,J.H.  
TITLE Method and reagent for the inhibition of grid

JOURNAL Patent: WO 0162911-A 2287 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
FEATURES  
source  
1. .30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
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1. .7  
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misc\_feature  
23. .29  
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misc\_feature  
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BASE COUNT 7 a 9 c 6 g 7 t 1 others  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGCTAGCTACAACGA 16  
:|||||  
Db 7 GGCTAGCTACAACGA 22

RESULT 13  
AX274719 30 bp DNA linear PAT 29-OCT-2001  
LOCUS  
DEFINITION Sequence 2288 from Patent WO0162911.  
ACCESSION AX274719  
VERSION AX274719.1 GI:16547458  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and Ellis, J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 2288 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
FEATURES  
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1. .30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
misc\_feature  
1. .7  
/note="2'-O-Methyl"  
misc\_feature  
23. .29  
/note="2'-O-Methyl"  
misc\_feature  
30  
/note="n stands for inverted deoxyabasic derivative"  
BASE COUNT 10 a 7 c 7 g 5 t 1 others  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGCTAGCTACAACGA 16  
:|||||  
Db 7 AGCTAGCTACAACGA 22

RESULT 14  
AX274720 30 bp DNA linear PAT 29-OCT-2001  
LOCUS  
DEFINITION Sequence 2289 from Patent WO0162911.  
ACCESSION AX274720  
VERSION AX274720.1 GI:16547459  
KEYWORDS

SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and Ellis, J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 2289 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
FEATURES  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
misc\_feature  
1. .7  
/note="2'-O-Methyl"  
misc\_feature  
23. .29  
/note="2'-O-Methyl"  
misc\_feature  
30  
/note="n stands for inverted deoxyabasic derivative"  
BASE COUNT 9 a 4 c 10 g 6 t 1 others  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGCTAGCTACAACGA 16  
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Db 7 AGCTAGCTACAACGA 22

RESULT 15  
AX274721 30 bp DNA linear PAT 29-OCT-2001  
LOCUS  
DEFINITION Sequence 2290 from Patent WO0162911.  
ACCESSION AX274721  
VERSION AX274721.1 GI:16547460  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and Ellis, J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 2290 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
FEATURES  
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1. .30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
misc\_feature  
1. .7  
/note="2'-O-Methyl"  
misc\_feature  
23. .29  
/note="2'-O-Methyl"  
misc\_feature  
30  
/note="n stands for inverted deoxyabasic derivative"  
BASE COUNT 9 a 4 c 10 g 6 t 1 others  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGCTAGCTACAACGA 16  
:|||||  
Db 7 AGCTAGCTACAACGA 22

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RESULT 16
AX274722 30 bp DNA linear PAT 29-OCT-2001
LOCUS AX274722
DEFINITION Sequence 2291 from Patent WO0162911.
ACCESSION AX274722
VERSION AX274722.1 GI:16547461
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Jarvis, T., von Carlwitzer, I., Mcswigen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 2291 30-AUG-2001; GLAXO GROUP LIMITED (GB)
RIBOZYME PHARMACEUTICALS, INC. (US) ;
FEATURES
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/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
misc_feature 1..7
/note="2'-O-Methyl"
misc_feature 23..29
/note="2'-O-Methyl"
misc_feature 30
/note="n stands for inverted deoxyabasic derivative"
BASE COUNT 8 a 7 c 10 g 4 t 1 others
ORIGIN
Query Match 97.5%; Score 15.6; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
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Db 7 GGGCTAGCTACACGA 22

RESULT 17
AR116975 31 bp DNA linear PAT 16-MAY-2001
LOCUS AR116975
DEFINITION Sequence 5 from patent US 6140055.
ACCESSION AR116975
VERSION AR116975.1 GI:14097881
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 31)
AUTHORS Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE Zymogenic nucleic acid detection methods and related kits
JOURNAL Patent: US 6140055-A 5 31-OCT-2000;
FEATURES
source 1..31
/organism="unknown"
BASE COUNT 10 a 7 c 7 g 7 t
ORIGIN
Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
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Db 8 AGGCTAGCTACACGA 23

RESULT 18
AR201827 31 bp DNA linear PAT 20-APR-2002
LOCUS AR201827
DEFINITION Sequence 42 from patent US 6361941.

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ACCESSION AR201827
VERSION AR201827.1 GI:20256366
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 31)
AUTHORS Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 42 26-MAR-2002;
FEATURES
source 1..31
/organism="unknown"
BASE COUNT 10 a 10 c 5 g 6 t
ORIGIN
Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
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Db 10 AGGCTAGCTACACGA 25

RESULT 19
AR201830 31 bp DNA linear PAT 20-APR-2002
LOCUS AR201830
DEFINITION Sequence 45 from patent US 6361941.
ACCESSION AR201830
VERSION AR201830.1 GI:20256369
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 31)
AUTHORS Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 45 26-MAR-2002;
FEATURES
source 1..31
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BASE COUNT 11 a 9 c 5 g 6 t
ORIGIN
Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
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Db 10 AGGCTAGCTACACGA 25

RESULT 20
AR201833 31 bp DNA linear PAT 20-APR-2002
LOCUS AR201833
DEFINITION Sequence 48 from patent US 6361941.
ACCESSION AR201833
VERSION AR201833.1 GI:20256372
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 31)
AUTHORS Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 48 26-MAR-2002;
FEATURES
source 1..31
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BASE COUNT 10 a 6 c 12 g 3 t
ORIGIN

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Query Match 97.5%; Score 15.6; DB 6; Length 31;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16  
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Db 9 GGGCTAGCTACACGA 24

RESULT 21  
LOCUS AR201836 31 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 51 from patent US 6361941.  
ACCESSION AR201836  
VERSION AR201836.1 GI:20256375  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
FEATURES  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
TITLE Catalytic nucleic acid-based diagnostic methods  
JOURNAL Patent: US 6361941-A 51 26-MAR-2002;  
FEATURES  
source 1. 31  
/organism="unknown"  
BASE COUNT 11 a 6 c 11 g 3 t  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16  
:|||||  
Db 9 AGGCTAGCTACACGA 24

RESULT 22  
LOCUS AR204371 31 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 5 from patent US 6365724.  
ACCESSION AR204371  
VERSION AR204371.1 GI:21501005  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
FEATURES  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
TITLE Zymogenic nucleic acid detection methods, and related molecules and kits  
JOURNAL Patent: US 6365724-A 5 02-APR-2002;  
FEATURES  
source 1. 31  
/organism="unknown"  
BASE COUNT 10 a 7 c 7 g 7 t  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16  
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Db 8 AGGCTAGCTACACGA 23

RESULT 23  
LOCUS AX220546 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5988 from Patent WO0159103.

ACCESSION AX220546  
VERSION AX220546.1 GI:15548270  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
FEATURES  
REFERENCE 1  
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5988 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source 1. 31  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
BASE COUNT 10 a 8 c 8 g 5 t  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16  
:|||||  
Db 8 GGGCTAGCTACACGA 23

RESULT 24  
LOCUS AX220547 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5989 from Patent WO0159103.  
ACCESSION AX220547  
VERSION AX220547.1 GI:15548271  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
FEATURES  
REFERENCE 1  
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5989 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
BASE COUNT 10 a 7 c 11 g 3 t  
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16  
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Db 8 GGGCTAGCTACACGA 23

RESULT 25  
LOCUS AX220548 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5990 from Patent WO0159103.  
ACCESSION AX220548  
VERSION AX220548.1 GI:15548272  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5990 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 9 a 8 c 6 g 8 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16  
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8 AGGCTAGCTACAACGA 23

Db

RESULT 26  
AX220549 31 bp DNA linear PAT 07-SEP-2001  
LOCUS  
DEFINITION Sequence 5991 from Patent WO0159103.  
ACCESSION AX220549  
VERSION AX220549.1 GI:15548273  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5991 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 11 a 7 c 8 g 5 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16  
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8 AGGCTAGCTACAACGA 23

Db

RESULT 27  
AX220550 31 bp DNA linear PAT 07-SEP-2001  
LOCUS  
DEFINITION Sequence 5992 from Patent WO0159103.  
ACCESSION AX220550  
VERSION AX220550.1 GI:15548274  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5992 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
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Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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8 GGGCTAGCTACAACGA 23

Db

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AX220551 31 bp DNA linear PAT 07-SEP-2001  
LOCUS  
DEFINITION Sequence 5993 from Patent WO0159103.  
ACCESSION AX220551  
VERSION AX220551.1 GI:15548275  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5993 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
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BASE COUNT 9 a 5 c 10 g 7 t

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Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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LOCUS  
DEFINITION Sequence 5994 from Patent WO0159103.  
ACCESSION AX220552  
VERSION AX220552.1 GI:15548276  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression  
Patent: WO 0159103-A 5994 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
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LOCUS  
DEFINITION  
Sequence 5995 from Patent W00159103.  
ACCESSION  
AX220553  
VERSION  
AX220553.1 GI:15548277  
KEYWORDS  
SOURCE  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS  
1  
Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE  
Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
Patent: WO 0159103-A 5995 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
location/Qualifiers

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BASE COUNT  
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ACCESSION  
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VERSION  
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KEYWORDS  
SOURCE  
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synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS  
1  
Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE  
Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
Patent: WO 0159103-A 5996 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

FEATURES  
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McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
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8 GGCTAGCTACACGA 23

RESULT 32  
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LOCUS  
DEFINITION  
Sequence 5997 from Patent W00159103.  
ACCESSION  
AX220555  
VERSION  
AX220555.1 GI:15548279  
KEYWORDS  
SOURCE  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS  
1  
Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE  
Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
Patent: WO 0159103-A 5997 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
location/Qualifiers

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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 33  
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LOCUS  
DEFINITION  
Sequence 5998 from Patent W00159103.  
ACCESSION  
AX220556  
VERSION  
AX220556.1 GI:15548280  
KEYWORDS  
SOURCE  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS  
1  
Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE  
Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
Patent: WO 0159103-A 5998 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
location/Qualifiers

FEATURES  
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Query Match 97.5%; Score 15.6; DB 6; Length 31;

Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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8 AGGCTAGCTACAACA 23

RESULT 38  
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LOCUS AX220561 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 6003 from Patent WO0159103.  
ACCESSION AX220561  
VERSION AX220561.1 GI:15548285

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blact, L., Mcswiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 6003 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blact, Lawrence (US) ;  
Mcswiggen, James (US) ; Chowrira, Bharat M. (US)

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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX220562 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 6004 from Patent WO0159103.  
ACCESSION AX220562  
VERSION AX220562.1 GI:15548286

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blact, L., Mcswiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 6004 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blact, Lawrence (US) ;  
Mcswiggen, James (US) ; Chowrira, Bharat M. (US)

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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 40  
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LOCUS AX220563 31 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 6005 from Patent WO0159103.  
ACCESSION AX220563  
VERSION AX220563.1 GI:15548287

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blact, L., Mcswiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 6005 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blact, Lawrence (US) ;  
Mcswiggen, James (US) ; Chowrira, Bharat M. (US)

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BASE COUNT 7 a 7 c 11 g 6 t  
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Query Match 97.5%; Score 15.6; DB 6; Length 31;

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Job time : 1009 secs

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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 05:18:03 ; Search time 151.5 Seconds

(without alignments)  
285.089 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16

Sequence: 1 rgcgtagctacaagca 16

Scoring table: IDENTITY\_NUC

Gap 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2722628

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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5	15.6	97.5	16	23	ABK09278	DNAzyme motif SEQ
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7	15.6	97.5	16	24	ABK22719	DNAzyme motif. Sy
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118	15.6	97.5	31	22	AAH96996	Human	Chk1	ribozym
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122	15.6	97.5	31	22	AAH97000	Human	Chk1	ribozym
123	15.6	97.5	31	22	AAH97001	Human	Chk1	ribozym
124	15.6	97.5	31	22	AAH97002	Human	Chk1	ribozym
125	15.6	97.5	31	22	AAH97003	Human	Chk1	ribozym
126	15.6	97.5	31	22	AAH97004	Human	Chk1	ribozym
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228	15.6	97.5	31	22	AAH97106	Human	Chk1	ribozym	301	15.6	97.5	31	22	AAH97179	Human	Chk1	ribozym
229	15.6	97.5	31	22	AAH97107	Human	Chk1	ribozym	302	15.6	97.5	31	22	AAH97180	Human	Chk1	ribozym
230	15.6	97.5	31	22	AAH97108	Human	Chk1	ribozym	303	15.6	97.5	31	22	AAH97181	Human	Chk1	ribozym
231	15.6	97.5	31	22	AAH97109	Human	Chk1	ribozym	304	15.6	97.5	31	22	AAH97182	Human	Chk1	ribozym
232	15.6	97.5	31	22	AAH97110	Human	Chk1	ribozym	305	15.6	97.5	31	22	AAH97183	Human	Chk1	ribozym
233	15.6	97.5	31	22	AAH97111	Human	Chk1	ribozym	306	15.6	97.5	31	22	AAH97184	Human	Chk1	ribozym
234	15.6	97.5	31	22	AAH97112	Human	Chk1	ribozym	307	15.6	97.5	31	22	AAH97185	Human	Chk1	ribozym
235	15.6	97.5	31	22	AAH97113	Human	Chk1	ribozym	308	15.6	97.5	31	22	AAH97186	Human	Chk1	ribozym
236	15.6	97.5	31	22	AAH97114	Human	Chk1	ribozym	309	15.6	97.5	31	22	AAH97187	Human	Chk1	ribozym
237	15.6	97.5	31	22	AAH97115	Human	Chk1	ribozym	310	15.6	97.5	31	22	AAH97188	Human	Chk1	ribozym
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240	15.6	97.5	31	22	AAH97118	Human	Chk1	ribozym	313	15.6	97.5	31	22	AAH97191	Human	Chk1	ribozym
241	15.6	97.5	31	22	AAH97119	Human	Chk1	ribozym	314	15.6	97.5	31	22	AAH97192	Human	Chk1	ribozym
242	15.6	97.5	31	22	AAH97120	Human	Chk1	ribozym	315	15.6	97.5	31	22	AAH97193	Human	Chk1	ribozym
243	15.6	97.5	31	22	AAH97121	Human	Chk1	ribozym	316	15.6	97.5	31	22	AAH97194	Human	Chk1	ribozym
244	15.6	97.5	31	22	AAH97122	Human	Chk1	ribozym	317	15.6	97.5	31	22	AAH97195	Human	Chk1	ribozym
245	15.6	97.5	31	22	AAH97123	Human	Chk1	ribozym	318	15.6	97.5	31	22	AAH97196	Human	Chk1	ribozym
246	15.6	97.5	31	22	AAH97124	Human	Chk1	ribozym	319	15.6	97.5	31	22	AAH97197	Human	Chk1	ribozym
247	15.6	97.5	31	22	AAH97125	Human	Chk1	ribozym	320	15.6	97.5	31	22	AAH97198	Human	Chk1	ribozym
248	15.6	97.5	31	22	AAH97126	Human	Chk1	ribozym	321	15.6	97.5	31	22	AAH97199	Human	Chk1	ribozym
249	15.6	97.5	31	22	AAH97127	Human	Chk1	ribozym	322	15.6	97.5	31	22	AAH97200	Human	Chk1	ribozym
250	15.6	97.5	31	22	AAH97128	Human	Chk1	ribozym	323	15.6	97.5	31	22	AAH97201	Human	Chk1	ribozym
251	15.6	97.5	31	22	AAH97129	Human	Chk1	ribozym	324	15.6	97.5	31	22	AAH97202	Human	Chk1	ribozym
252	15.6	97.5	31	22	AAH97130	Human	Chk1	ribozym	325	15.6	97.5	31	22	AAH97203	Human	Chk1	ribozym
253	15.6	97.5	31	22	AAH97131	Human	Chk1	ribozym	326	15.6	97.5	31	22	AAH97204	Human	Chk1	ribozym
254	15.6	97.5	31	22	AAH97132	Human	Chk1	ribozym	327	15.6	97.5	31	22	AAH97205	Human	Chk1	ribozym
255	15.6	97.5	31	22	AAH97133	Human	Chk1	ribozym	328	15.6	97.5	31	22	AAH97206	Human	Chk1	ribozym
256	15.6	97.5	31	22	AAH97134	Human	Chk1	ribozym	329	15.6	97.5	31	22	AAH97207	Human	Chk1	ribozym
257	15.6	97.5	31	22	AAH97135	Human	Chk1	ribozym	330	15.6	97.5	31	22	AAH97208	Human	Chk1	ribozym
258	15.6	97.5	31	22	AAH97136	Human	Chk1	ribozym	331	15.6	97.5	31	22	AAH97209	Human	Chk1	ribozym
259	15.6	97.5	31	22	AAH97137	Human	Chk1	ribozym	332	15.6	97.5	31	22	AAH97210	Human	Chk1	ribozym
260	15.6	97.5	31	22	AAH97138	Human	Chk1	ribozym	333	15.6	97.5	31	22	AAH97211	Human	Chk1	ribozym
261	15.6	97.5	31	22	AAH97139	Human	Chk1	ribozym	334	15.6	97.5	31	22	AAH97212	Human	Chk1	ribozym
262	15.6	97.5	31	22	AAH97140	Human	Chk1	ribozym	335	15.6	97.5	31	22	AAH97213	Human	Chk1	ribozym
263	15.6	97.5	31	22	AAH97141	Human	Chk1	ribozym	336	15.6	97.5	31	22	AAH97214	Human	Chk1	ribozym
264	15.6	97.5	31	22	AAH97142	Human	Chk1	ribozym	337	15.6	97.5	31	22	AAH97215	Human	Chk1	ribozym
265	15.6	97.5	31	22	AAH97143	Human	Chk1	ribozym	338	15.6	97.5	31	22	AAH97216	Human	Chk1	ribozym
266	15.6	97.5	31	22	AAH97144	Human	Chk1	ribozym	339	15.6	97.5	31	22	AAH97217	Human	Chk1	ribozym
267	15.6	97.5	31	22	AAH97145	Human	Chk1	ribozym	340	15.6	97.5	31	22	AAH97218	Human	Chk1	ribozym
268	15.6	97.5	31	22	AAH97146	Human	Chk1	ribozym	341	15.6	97.5	31	22	AAH97219	Human	Chk1	ribozym
269	15.6	97.5	31	22	AAH97147	Human	Chk1	ribozym	342	15.6	97.5	31	22	AAH97220	Human	Chk1	ribozym
270	15.6	97.5	31	22	AAH97148	Human	Chk1	ribozym	343	15.6	97.5	31	22	AAH97221	Human	Chk1	ribozym
271	15.6	97.5	31	22	AAH97149	Human	Chk1	ribozym	344	15.6	97.5	31	22	AAH97222	Human	Chk1	ribozym
272	15.6	97.5	31	22	AAH97150	Human	Chk1	ribozym	345	15.6	97.5	31	22	AAH97223	Human	Chk1	ribozym
273	15.6	97.5	31	22	AAH97151	Human	Chk1	ribozym	346	15.6	97.5	31	22	AAH97224	Human	Chk1	ribozym
274	15.6	97.5	31	22	AAH97152	Human	Chk1	ribozym	347	15.6	97.5	31	22	AAH97225	Human	Chk1	ribozym
275	15.6	97.5	31	22	AAH97153	Human	Chk1	ribozym	348	15.6	97.5	31	22	AAH97226	Human	Chk1	ribozym
276	15.6	97.5	31	22	AAH97154	Human	Chk1	ribozym	349	15.6	97.5	31	22	AAH97227	Human	Chk1	ribozym
277	15.6	97.5	31	22	AAH97155	Human	Chk1	ribozym	350	15.6	97.5	31	22	AAH97228	Human	Chk1	ribozym
278	15.6	97.5	31	22	AAH97156	Human	Chk1	ribozym	351	15.6	97.5	31	22	AAH97229	Human	Chk1	ribozym
279	15.6	97.5	31	22	AAH97157	Human	Chk1	ribozym	352	15.6	97.5	31	22	AAH97230	Human	Chk1	ribozym
280	15.6	97.5	31	22	AAH97158	Human	Chk1	ribozym	353	15.6	97.5	31	22	AAH97231	Human	Chk1	ribozym
281	15.6	97.5	31	22	AAH97159	Human	Chk1	ribozym	354	15.6	97.5	31	22	AAH97232	Human	Chk1	ribozym
282	15.6	97.5	31	22	AAH97160	Human	Chk1	ribozym	355	15.6	97.5	31	22	AAH97233	Human	Chk1	ribozym
283	15.6	97.5	31	22	AAH97161	Human	Chk1	ribozym	356	15.6	97.5	31	22	AAH97234	Human	Chk1	ribozym
284	15.6	97.5	31	22	AAH97162	Human	Chk1	ribozym	357	15.6	97.5	31	22	AAH97235	Human	Chk1	ribozym
285	15.6	97.5	31	22	AAH97163	Human	Chk1	ribozym	358	15.6	97.5	31	22	AAH97236	Human	Chk1	ribozym
286	15.6	97.5	31	22	AAH97164	Human	Chk1	ribozym	359	15.6	97.5	31	22	AAH97237	Human	Chk1	ribozym
287	15.6	97.5	31	22	AAH97165	Human	Chk1	ribozym	360	15.6	97.5	31	22	AAH97238	Human	Chk1	ribozym
288	15.6	97.5	31	22	AAH97166	Human	Chk1	ribozym	361	15.6	97.5	31	22	AAH97239	Human	Chk1	ribozym
289	15.6	97.5	31	22	AAH97167	Human	Chk1	ribozym	362	15.6	97.5	31	22	AAH97240	Human	Chk1	ribozym
290	15.6	97.5	31	22	AAH97168	Human	Chk1	ribozym	363	15.6	97.5	31	22	AAH97241	Human	Chk1	ribozym
291	15.6	97.5	31	22	AAH97169	Human	Chk1	ribozym	364	15.6	97.5	31	22	AAH97242	Human	Chk1	ribozym
292	15.6	97.5	31	22	AAH97170	Human	Chk1	ribozym	365	15.6	97.5	31	22	AAH97243	Human	Chk1	ribozym
293	15.6	97.5	31	22	AAH97171	Human	Chk1	ribozym	366	15.6	97.5	31	22	AAH97244	Human	Chk1	ribozym
294	15.6	97.5	31	22	AAH97172	Human	Chk1	ribozym	367	15.6	97.5	31	22	AAH97245	Human	Chk1	ribozym
295	15.6	97.5	31	22	AAH97173	Human	Chk1	ribozym	368	15.6	97.5	31	22	AAH97246	Human	Chk1	ribozym
296	15.6	97.5	31	22	AAH97174	Human	Chk1	ribozym	369	15.6	97.5	31	22	AAH97247	Human	Chk1	ribozym
297	15.6	97.5	31	22	AAH97175	Human	Chk1	ribozym	370	15.6	97.5	31	22	AAH97248	Human	Chk1	ribozym
298	15.6	97.5	31	22	AAH97176	Human	Chk1	ribozym	371	15.6	97.5	31	22	AAH97249	Human	Chk1	ribozym
299	15.6	97.5	31	22	AAH97177	Human	Chk1	ribozym	372	15.6	97.5	31	22	AAH97250	Human	Chk1	ribozym
300	15.6	97.5	31	22	AAH97178	Human	Chk1	ribozym	373	15.6	97.5	31	22	AAH97251	Human	Chk1	ribozym









958	15.6	97.5	31	23	ABK06477	Human NOGO DNzyme
959	15.6	97.5	31	23	ABK06478	Human NOGO DNzyme
960	15.6	97.5	31	23	ABK06479	Human NOGO DNzyme
961	15.6	97.5	31	23	ABK06480	Human NOGO DNzyme
962	15.6	97.5	31	23	ABK06481	Human NOGO DNzyme
963	15.6	97.5	31	23	ABK06482	Human NOGO DNzyme
964	15.6	97.5	31	23	ABK06483	Human NOGO DNzyme
965	15.6	97.5	31	23	ABK06484	Human NOGO DNzyme
966	15.6	97.5	31	23	ABK06485	Human NOGO DNzyme
967	15.6	97.5	31	23	ABK06486	Human NOGO DNzyme
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971	15.6	97.5	31	23	ABK06490	Human NOGO DNzyme
972	15.6	97.5	31	23	ABK06491	Human NOGO DNzyme
973	15.6	97.5	31	23	ABK06492	Human NOGO DNzyme
974	15.6	97.5	31	23	ABK06493	Human NOGO DNzyme
975	15.6	97.5	31	23	ABK06494	Human NOGO DNzyme
976	15.6	97.5	31	23	ABK06495	Human NOGO DNzyme
977	15.6	97.5	31	23	ABK06496	Human NOGO DNzyme
978	15.6	97.5	31	23	ABK06497	Human NOGO DNzyme
979	15.6	97.5	31	23	ABK06498	Human NOGO DNzyme
980	15.6	97.5	31	23	ABK06499	Human NOGO DNzyme
981	15.6	97.5	31	23	ABK06500	Human NOGO DNzyme
982	15.6	97.5	31	23	ABK06501	Human NOGO DNzyme
983	15.6	97.5	31	23	ABK06502	Human NOGO DNzyme
984	15.6	97.5	31	23	ABK06503	Human NOGO DNzyme
985	15.6	97.5	31	23	ABK06504	Human NOGO DNzyme
986	15.6	97.5	31	23	ABK06505	Human NOGO DNzyme
987	15.6	97.5	31	23	ABK06506	Human NOGO DNzyme
988	15.6	97.5	31	23	ABK06507	Human NOGO DNzyme
989	15.6	97.5	31	23	ABK06508	Human NOGO DNzyme
990	15.6	97.5	31	23	ABK06509	Human NOGO DNzyme
991	15.6	97.5	31	23	ABK06510	Human NOGO DNzyme
992	15.6	97.5	31	23	ABK06511	Human NOGO DNzyme
993	15.6	97.5	31	23	ABK06512	Human NOGO DNzyme
994	15.6	97.5	31	23	ABK06513	Human NOGO DNzyme
995	15.6	97.5	31	23	ABK06514	Human NOGO DNzyme
996	15.6	97.5	31	23	ABK06515	Human NOGO DNzyme
997	15.6	97.5	31	23	ABK06516	Human NOGO DNzyme
998	15.6	97.5	31	23	ABK06517	Human NOGO DNzyme
999	15.6	97.5	31	23	ABK06518	Human NOGO DNzyme
1000	15.6	97.5	31	25	ABL53699	Prostate cancer ma

## ALIGNMENTS

```

RESULT 1
AAV82953
ID   AAV82953 standard; DNA; 16 BP.
XX
AC   AAV82953;
XX
DT   05-MAR-1999 (first entry)
XX
DE   Enzymatic DNA core motif region.
XX
KW   Enzyme; catalysis; cleavage; target; pharmaceutical; medical; substrate;
XX   regulator; detergent; dental hygiene; meat tenderizer; ss.
XX
OS   Synthetic.
XX
PN   WO9849346-A1.
XX
PD   05-NOV-1998.
XX
PF   29-APR-1998; 98WO-US08677.
XX
PR   29-APR-1997; 97US-0045228.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX

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PI   Breaker RR, Joyce GF;
XX
DR   WPI; 1999-034670/03.
XX
PT   New catalytic DNA molecules - having site-specific endonuclease
PT   activity in a substrate nucleic acid, used for cleaving target
PI   nucleic acid sequences
XX
PS   Claim 1; Page 96; 161pp; English.
XX
CC   This sequence is used in a method which involves the production of
CC   catalytic DNA molecules which can be used for cleaving target nucleic
CC   acid molecules. Such DNA molecules can be used in pharmaceutical and
CC   medical products (e.g. for wound debridement, clot dissolution), as well
CC   as in household items (e.g. detergents, dental hygiene products, meat
CC   tenderizers). Other suitable substrates include those comprising or
CC   produced by picornaviruses, hepadnaviridae, (e.g. HBV, HCV),
CC   papillomaviruses (e.g. HPV), gammaherpesvirinae (e.g. EBV),
CC   lymphocryptoviruses, leukemia viruses (e.g. HTLV-1 and -11),
CC   flaviviruses, togaviruses, herpesviruses (including alphaherpesvirus
CC   and betaherpesviruses), cytomegaloviruses (CMV), influenza viruses,
CC   viruses and retroviruses contributing to immunodeficiency diseases and
CC   syndromes (e.g. HIV-1 and -2), simian and feline immunodeficiency
CC   viruses and bovine leukemia viruses. They can also be used as regulators
CC   of gene expression.
XX
SQ   Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
XX
Query Match          97.5%; Score 15.6; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy   1 RGGCTAGCTACACGA 16
Db   1 RGGCTAGCTACACGA 16
XX
RESULT 2
AAC63474
ID   AAC63474 standard; DNA; 16 BP.
XX
AC   AAC63474;
XX
DT   07-FEB-2001 (first entry)
XX
DE   DNzyme catalytic core #2.
XX
KW   Antisense; ribozyme; DNzyme; ss.
XX
OS   Unidentified.
XX
PN   WO200060115-A2.
XX
PD   12-OCT-2000.
XX
PF   27-MAR-2000; 2000WO-US07920.
XX
PR   02-APR-1999; 99US-0127529.
XX
PA   (CITY ) CITY OF HOPE.
XX
PI   Rossi J, Riggs A, Scherr M;
XX
DR   WPI; 2000-665016/64.
XX
PT   Identifying sites on a target or in vitro-synthesized RNA accessible to
PT   antisense, ribozyme, or DNzyme binding comprises incubating
PT   hybridizing the target RNA with an antisense oligodeoxynucleotide,
PT   ribozymes or DNzymes -
XX
PS   Disclosure; Page 7; 38pp; English.
XX
CC   The present invention relates to a method for identifying sites on a

```

CC target RNA which are accessible to pairing by antisense DNA, ribozymes or  
CC DNazymes. The present sequence is a DNazyme catalytic core sequence.  
CC In the method of the present invention the target sequence is incubated  
CC with DNazymes, antisense oligonucleotides or ribozymes (such as the  
CC present sequence). Any antisense oligonucleotide, ribozyme or DNazyme  
CC which is complementary to an accessible site in the target sequence  
CC hybridizes to that site and the sequence is cleaved. The cleavage  
CC products can then be detected to identify the accessible binding sites.

XX  
SQ Sequence 16 BP; 6 A; 4 C; 4 G; 2 T; 0 other;

Query Match 97.5%; Score 15.6; DB 21; Length 16;  
Best Local Similarity 93.8%; Pred. No. 34;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 1 AGGCTAGCTACACGA 16

## RESULT 3

AAC63475  
ID AAC63475 standard; DNA; 16 BP.

XX AAC63475;

XX 07-FEB-2001 (first entry)

XX DNazyme catalytic core #3.

XX Antisense; ribozyme; DNazyme; ss.

XX Unidentified.

XX WO200060115-A2.

XX 12-OCT-2000.

XX 27-MAR-2000; 2000WO-US07920.

XX 02-APR-1999; 99US-0127529.

XX (CITY) CITY OF HOPE.

XX Rossi J, Riggs A, Scherr M;

XX WPI; 2000-665016/64.

XX Identifying sites on a target or in vitro-synthesized RNA accessible to

PT antisense, ribozyme, or DNazyme binding comprises incubating

PT hybridizing the target RNA with an antisense oligodeoxynucleotides,

PT ribozymes or DNazymes -

XX Disclosure; Page 7; 38pp; English.

XX The present invention relates to a method for identifying sites on a  
CC target RNA which are accessible to pairing by antisense DNA, ribozymes or  
CC DNazymes. The present sequence is a DNazyme catalytic core sequence.  
CC In the method of the present invention the target sequence is incubated  
CC with DNazymes, antisense oligonucleotides or ribozymes (such as the  
CC present sequence). Any antisense oligonucleotide, ribozyme or DNazyme  
CC which is complementary to an accessible site in the target sequence  
CC hybridizes to that site and the sequence is cleaved. The cleavage  
CC products can then be detected to identify the accessible binding sites.

XX Sequence 16 BP; 5 A; 4 C; 5 G; 2 T; 0 other;

Query Match 97.5%; Score 15.6; DB 21; Length 16;  
Best Local Similarity 93.8%; Pred. No. 34;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 1 AGGCTAGCTACACGA 16

Db 1 GGCTAGCTACACGA 16

## RESULT 4

ABA02749  
ID ABA02749 standard; DNA; 16 BP.

XX ABA02749;

XX 12-FEB-2002 (first entry)

XX DNazyme motif SEQ ID NO 21.

XX Nucleic acid sensor molecule; detection; infection; disease diagnosis;

XX physiological abnormality; electronic; signalling molecule; ribozyme;

XX nucleoside analogue; DNazyme; ss.

XX Synthetic.

XX WO200166721-A2.

XX 13-SEP-2001.

XX 06-MAR-2001; 2001WO-US07163.

XX 06-MAR-2000; 2000US-187128P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Usman N, McSwiggen JA, Zinnen S, Selwert S, Haerberl P;

XX Chowrira B, Blatt L;

XX WPI; 2001-616242/71.

XX New nucleic acid sensor molecule useful in diagnostic applications,

PT nucleic acid-based electronics and functional genomics, comprises an

PT enzymatic nucleic acid and one or more sensors -

XX Disclosure; Fig 4; 115pp; English.

XX The invention relates to a nucleic acid sensor molecule (I) comprising an  
CC enzymatic nucleic acid component and one or more sensor components. (I)  
CC is useful in diagnostic applications to identify the presence of genes  
CC and/or gene products indicative of a particular genotype and/or  
CC phenotype, e.g. a disease state or infection and for diagnosis of disease  
CC states or physiological abnormalities related to the expression of viral,  
CC bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based  
CC electronics, for the detection of specific target signalling molecules,  
CC in assays to assess the specificity, toxicity and effectiveness of  
CC various small molecules, nucleoside analogues or non-nucleic acid drugs  
CC or for detection of pathogens, biochemicals, organic or inorganic  
CC compounds. The present sequence is that of a DNazyme motif of the  
CC invention.

XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;

Query Match 97.5%; Score 15.6; DB 22; Length 16;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

## RESULT 5

AAH97756  
ID AAH97756 standard; DNA; 16 BP.

XX AAH97756;

XX 09-OCT-2001 (first entry)

DE DNazyme ribozyme motif SEQ ID NO: 3186.  
 XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;  
 KW RNA cleavage; cancer; ss.  
 XX Unidentified.  
 OS  
 FN WO200157206-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 02-FEB-2001; 2001WO-US03504.  
 XX  
 PR 03-FEB-2000; 2000US-0179983.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (FATT/) FATTAEY A R.  
 XX  
 PI Fattaeay AR, Jarvis T, McSwiggen J, Booher RN, Holman PS;  
 DR WPI; 2001-496922/54.  
 XX  
 PT Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid  
 PT molecules, which downregulate expression of a checkpoint kinase-1  
 PT gene, useful for treating colorectal, lung, breast or prostate cancers  
 PT -  
 PS Claim 8; Fig 5; 115pp; English.  
 XX  
 CC The present invention provides nucleic acid molecules capable of  
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)  
 CC gene. These may be antisense or ribozyme sequences, and are useful in the  
 CC treatment of diseases associated with conditions affected by Chk1 levels,  
 CC including cancer. The present sequence is an oligonucleotide described in  
 CC the exemplification of the invention.  
 CC  
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 XX  
 QY Query Match 97.5%; Score 15.6; DB 22; Length 16;  
 XX Best Local Similarity 100.0%; Pred. No. 34;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 RGCTAGCTACAACGA 16  
 1 RGCTAGCTACAACGA 16  
 XX  
 RESULT 6  
 ABRK09278  
 ID ABRK09278 standard; DNA; 16 BP.  
 XX  
 AC ABRK09278;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE DNazyme motif.  
 XX  
 KW Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hampered ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200159103-A2.

XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US04273.  
 XX  
 PR 11-FEB-2000; 2000US-181797P.  
 PR 28-FEB-2000; 2000US-185516P.  
 PR 06-MAR-2000; 2000US-187128P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 PI Blatt L, McSwiggen J, Chowrira BM;  
 DR WPI; 2001-607195/69.  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,  
 PT and central nervous system injury -  
 XX  
 PS Disclosure; Fig 5; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOCO).  
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN  
 CC motif) or an amberszyme (cleaving RNA with an NGN triplex), a zinzyme  
 CC (cleaving RNA with a VXY motif). The CD20-targeting nucleic acid is used  
 CC to cleave RNA of CD20 in the presence of a divalent cation that is  
 CC preferably Mg<sup>2+</sup>. Furthermore, it may be contacted with a cell to reduce  
 CC CD20 activity of the cell and treat a patient having a further condition  
 CC associated with the level of CD20. The treatment may further comprise the  
 CC use of one or more therapies. In particular, the CD20 targeting  
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell  
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky  
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human  
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),  
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune  
 CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting  
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a  
 CC divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the nucleic acid  
 CC may be contacted with a cell to reduce NOGO activity of the cell and  
 CC treat a patient having a condition associated with the level of NOGO. The  
 CC treatment may further comprise the use of one or more therapies.  
 CC In particular, the NOGO-targeting nucleic acid may be used to treat  
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,  
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The  
 CC present sequence is a DNazyme molecule of the invention.  
 CC  
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 XX  
 QY Query Match 97.5%; Score 15.6; DB 23; Length 16;  
 XX Best Local Similarity 100.0%; Pred. No. 34;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 RGCTAGCTACAACGA 16  
 1 RGCTAGCTACAACGA 16  
 XX  
 RESULT 7  
 ABRK1076  
 ID ABRK1076 standard; DNA; 16 BP.  
 XX

AC ABR61076;  
 XX  
 XX 02-JUL-2002 (first entry)  
 DE  
 XX Human CLCA1 gene enzymatic nucleic acid #5445.  
 XX  
 DE Human CLCA1 gene enzymatic nucleic acid #5445.  
 XX  
 DE Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KW antiinflammatory; chronic obstructive pulmonary disease, COPD; asthma;  
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KW acetylcysteine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200211674-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 09-AUG-2001; 2001WO-US24970.  
 XX  
 PR 09-AUG-2000; 2000US-224383P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (SYNT ) SYNTX USA LLC.  
 PA (THOM/) THOMPSON J.  
 XX  
 PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE,  
 PI Grube A;  
 XX  
 DR WPI; 2002-217145/27.  
 XX  
 PT Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma  
 XX  
 PS Disclosure; Fig 4; 152pp; English.  
 XX  
 CC The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition.  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention.  
 XX  
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 OY  
 Query Match 97.5%; Score 15.6; DB 24; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RGGCTAGCTACACGA 16  
 Db 1 RGGCTAGCTACACGA 16  
 RESULT 8  
 ABR22719  
 ID ABR22719 standard; RNA; 16 BP.  
 XX  
 AC ABR22719;  
 XX  
 DT 09-APR-2002 (first entry)

XX  
 DE DNazyme motif.  
 XX  
 XX Human; hammerhead ribozyme; cytosolic; antitumor; antidiabetic;  
 KW ophthalmological; antiarthritic; antiproliferative; virucide; osteoplastic;  
 KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 KW angiodioma of tuberous sclerosis; port-wine stain; wound healing;  
 KW Sturge Weber syndrome; Kippel-Trenauay-Weber syndrome; leukaemia; ss;  
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;  
 KW amberyze.  
 XX  
 OS Synthetic.  
 XX  
 PN WO20018124-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 16-MAY-2001; 2001WO-US15866.  
 XX  
 PR 16-MAY-2000; 2000US-0572021.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM,  
 PI WPI; 2002-082995/11.  
 XX  
 DR Novel polynucleotide which down regulates expression of Ets-related  
 PT gene, useful for treating cancer, diabetic retinopathy, macular  
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber  
 PT syndrome  
 XX  
 PS Disclosure; Figure 5; 149pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule (I) which down regulates  
 CC expression of an Ets-related gene (ERG). (I) is useful for treating  
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,  
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca  
 CC vulgaris, angiodioma of tuberous sclerosis, port-wine stains, Sturge  
 CC Weber syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-rendu  
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 CC treating a patient having a condition associated with the level of ERG,  
 CC by contacting cells of the patient with (I) under conditions suitable for  
 CC the treatment. The method comprises the use of one or more therapies  
 CC under conditions suitable for the treatment. Leukaemia or tumour  
 CC angiogenesis is treated by administering (I) to the patient in  
 CC conjunction with one or more of other therapies such as radiation or  
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and  
 CC diseases related to the expression of ERG, and as diagnostic tool to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of ERG RNA in a cell. (I) is useful for specifically  
 CC targeting genes that share homology with ERG gene or ERG fusion genes.  
 CC ABR17354-ABR22719 represent nucleic acids, including antisense and  
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
 CC related PCR primers of the invention.  
 XX  
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 OY  
 Query Match 97.5%; Score 15.6; DB 24; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RGGCTAGCTACACGA 16  
 Db 1 RGGCTAGCTACACGA 16

RESULT 9  
 ID ACA10109 standard; DNA; 16 BP.  
 AC ACA10109;  
 XX  
 XX 03-JUN-2003 (first entry)  
 DE Necrosis factor kappa B (NFkB) modulating DNazyme motif.  
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;  
 KW G-cleaver; amberyze; cancer; REL-A activity; breast cancer;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection;  
 KW ss.  
 OS Synthetic.  
 XX  
 XX US200217568-A1.  
 XX  
 XX 28-NOV-2002.  
 XX  
 XX 23-MAY-2001; 2001US-0864785.  
 XX  
 XX 15-AUG-1994; 94US-0291932.  
 XX 07-DEC-1992; 92US-0987132.  
 XX 18-MAY-1994; 94US-0245466.  
 XX 23-DEC-1996; 96US-0777916.  
 XX  
 XX (STIN/) STINCHOMB D T.  
 XX (MCSW/) MCSWIGEN J.  
 XX (DRAP/) DRAPER K G.  
 XX  
 XX Stinchcomb DT, Mcswigen J, Draper KG;  
 PI  
 DR WPI; 2003-340953/32.  
 XX  
 XX Novel enzymatic nucleic acid molecules which down regulates expression  
 PT of a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases -  
 XX  
 XX Fig 4; SEQ ID NO 3928; 72pp; English.  
 XX  
 XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberyze  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury

CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents a motif of an enzymatic nucleic acid  
 CC used to modulate the function of a necrosis factor kappa B sub-unit.  
 XX  
 XX SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;  
 XX  
 XX Query Match 97.5%; Score 15.6; DB 25; Length 16;  
 XX Best Local Similarity 100.0%; Pred. No. 34;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 RGCGTACGTACACGA 16  
 XX 1  
 XX DB 1 RGCGTACGTACACGA 16  
 XX  
 XX RESULT 10  
 XX AB258432  
 XX ID AB258432 standard; DNA; 16 BP.  
 XX  
 XX AC AB258432;  
 XX  
 XX DT 08-MAY-2003 (first entry)  
 XX  
 XX DE DNazyme motif.  
 XX  
 XX DNazyme; enzymatic nucleic acid; enzyme; transporter; drug  
 XX delivery; cytostatic; virucide; gene therapy; ss.  
 XX  
 XX OS Synthetic.  
 XX  
 XX WO2003008628-A2.  
 XX  
 XX 30-JAN-2003.  
 XX  
 XX 22-JUL-2002; 2002WO-US23324.  
 XX  
 XX 20-JUL-2001; 2001US-306995P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Beigelman L, Azhayer A, Azhayera E;  
 PI  
 DR WPI; 2003-247828/25.  
 XX  
 XX New transporter compounds useful for delivering molecules into  
 PT biological system such as cells, and for treating cancer and viral  
 PT infections -  
 XX  
 XX Disclosure; Fig 4; 88pp; English.  
 XX  
 XX The present sequence is an example of a DNazyme, an enzymatic  
 CC nucleic acid (ENA) that does not require the presence of a 2'-OH  
 CC group for its activity. DNazymes can be used as the ENA moiety in  
 CC novel ENA peptide conjugates (I) of the invention that facilitate  
 CC delivery of molecules into biological systems, such as cells. The  
 CC peptide part of the conjugate is typically a fusogenic peptide such  
 CC as a peptide given in ABP72298-ABP72305. The conjugates can be  
 CC used to treat a cancer patient, where the cancer is breast, lung,  
 CC colorectal, brain, oesophageal, stomach, bladder, pancreas, cervix,  
 CC head and neck or ovary cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer, or to treat a virus infection, where  
 CC the virus is HIV, hepatitis B virus, hepatitis C virus,  
 CC cytomegalovirus, Rous sarcoma virus, herpes simplex virus,  
 CC poliovirus, influenza virus, rhinovirus, west nile virus, Ebola  
 CC virus, foot and mouth disease virus or papilloma virus (all  
 CC claimed). (I) are useful for introducing nucleosides,  
 CC nucleosides, nucleic acid molecules, lipids, peptides, proteins  
 CC and/or non-nucleosidic small molecules into a cell and to detect  
 CC the presence of a target molecule in a biological system such as  
 CC tissue, cell or cell lysate. They are useful as diagnostic tools  
 CC to examine genetic drift and mutations within diseased cells or to

CC detect the presence of a disease-related RNA in a cell.  
XX  
SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;

Query Match 97.5%; Score 15.6; DB 25; Length 16;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
DB 1 RGGCTAGCTACACGA 16

## RESULT 11

ABZ66525  
ID ABZ66525 standard; RNA; 27 BP.

AC ABZ66525;

DT 21-MAR-2003 (first entry)

DE Human HER2 synthetic DNAzyme #1.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;  
KM anti-rheumatic; cancer; AIDS; ss.

OS Homo sapiens.

XX WO200297114-A2.

PD 05-DEC-2002.

PF 29-MAY-2002; 2002WO-US16840.

PR 29-MAY-2001; 2001US-294140P.

PR 06-JUN-2001; 2001US-296249P.

PR 10-SEP-2001; 2001US-318471P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Mcawiggen J;

DR WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX Claim 3; Page 153; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosolic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66588 represent human ribozymes of the  
CC invention.

XX Sequence 27 BP; 6 A; 6 C; 10 G; 2 T; 3 U; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 27;

Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
DB 6 AGGCTAGCTACACGA 21

## RESULT 12

ABZ66527  
ID ABZ66527 standard; RNA; 27 BP.

AC ABZ66527;

DT 21-MAR-2003 (first entry)

DE Human HER2 synthetic DNAzyme #3.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;  
KM anti-rheumatic; cancer; AIDS; ss.

OS Homo sapiens.

XX WO200297114-A2.

PD 05-DEC-2002.

PF 29-MAY-2002; 2002WO-US16840.

PR 29-MAY-2001; 2001US-294140P.

PR 06-JUN-2001; 2001US-296249P.

PR 10-SEP-2001; 2001US-318471P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Mcawiggen J;

DR WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX Claim 3; Page 153; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosolic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66588 represent human ribozymes of the  
CC invention.

XX Sequence 27 BP; 11 A; 8 C; 6 G; 2 T; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 27;  
Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
DB 6 AGGCTAGCTACACGA 21

## RESULT 13

AAZ34361  
ID AAZ34361 standard; DNA; 29 BP.

AC AAZ34361;

DT 14-DEC-1999 (first entry)

XX Nucleic acid-based diagnostic exemplification oligonucleotide #23.

XX Catalytic nucleic acid-based diagnostic method; determination; AIDS;  
 KW mutation; ribozyme; target; cleavage; amplification; PCR primer;  
 KW probe; cancer; human immune deficiency virus; cystic fibrosis; HIV; ss.  
 XX Synthetic.  
 XX WO9950452-A1.  
 XX PN 07-OCT-1999.  
 XX PD 16-MAR-1999; 99WO-IB00848.  
 XX PF 27-MAR-1999; 98US-0079651.  
 XX PR (JOHN ) JOHNSON & JOHNSON RES PTY LTD.  
 XX PA Todd AV, Fuery CJ, Cairns MJ;  
 XX PI WPI; 1999-591332/50.  
 XX DR  
 XX PT Detecting diseases associated with a known mutation by amplification  
 XX and cleavage with catalytic nucleic acids, particularly for cancer,  
 XX human immune deficiency virus and cystic fibrosis  
 XX  
 XX Disclosure; Page 20; 57pp; English.  
 XX PS  
 XX The present invention describes a method for determining whether a  
 XX subject is afflicted with a disorder characterised by the presence of  
 XX a known nucleic acid. The method comprises: (i) amplifying, in an  
 XX isolated sample from the subject, the nucleic acid segment that, in an  
 XX affected individual contains (A), (ii) treating the amplicons with a  
 XX catalytic nucleic acid (I) that specifically recognizes and cleaves a  
 XX target sequence present in either the mutated or wild-type segments,  
 XX but not in both; and (iii) detecting any cleavage caused by (I). Step  
 XX (ii) may be performed concurrently with (i). The method is specifically  
 XX used to diagnose cancer (especially), acquired immune deficiency  
 XX syndrome and cystic fibrosis. (i) recognises as few as two bp to create  
 XX a cleavage site (contrast at least 4 bp required by enzymes used in  
 XX restriction fragment length polymorphism (RFLP) analysis); such sites  
 XX occur more frequently than restriction enzyme sites, and mismatched  
 XX primers can be used to induce cleavage sites for (I). The method is  
 XX potentially more flexible than RFLP and does not require any enzymes or  
 XX toxic compounds. AA23439 to AA234450 represent oligonucleotide  
 XX sequences used in the exemplification of the present invention.  
 XX  
 XX Sequence 29 BP; 10 A; 5 C; 10 G; 3 T; 1 other;  
 XX SQ  
 XX Query Match 97.5%; Score 15.6; DB 20; Length 29;  
 XX Best Local Similarity 93.8%; Pred. No. 35;  
 XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 RGGCTAGCTACACGA 16  
 XX :|||||  
 XX DB 8 AGGCTAGCTACACGA 23  
 XX  
 XX RESULT 14  
 XX AA234363  
 XX ID AA234363 standard; DNA; 29 BP.  
 XX AC AA234363;  
 XX XX  
 XX DT 14-DEC-1999 (first entry)  
 XX XX  
 XX DE Nucleic acid-based diagnostic exemplification oligonucleotide #25.  
 XX XX  
 XX KW Catalytic nucleic acid-based diagnostic method; determination; AIDS;  
 XX mutation; ribozyme; target; cleavage; amplification; PCR primer;  
 XX probe; cancer; human immune deficiency virus; cystic fibrosis; HIV; ss.  
 XX XX  
 XX OS Synthetic.  
 XX XX

PN WO9950452-A1.  
 XX PD 07-OCT-1999.  
 XX XX 16-MAR-1999; 99WO-IB00848.  
 XX PF 27-MAR-1999; 98US-0079651.  
 XX PR (JOHN ) JOHNSON & JOHNSON RES PTY LTD.  
 XX PA Todd AV, Fuery CJ, Cairns MJ;  
 XX PI WPI; 1999-591332/50.  
 XX DR  
 XX PT Detecting diseases associated with a known mutation by amplification  
 XX and cleavage with catalytic nucleic acids, particularly for cancer,  
 XX human immune deficiency virus and cystic fibrosis  
 XX  
 XX Disclosure; Page 20; 57pp; English.  
 XX PS  
 XX The present invention describes a method for determining whether a  
 XX subject is afflicted with a disorder characterised by the presence of  
 XX a known nucleic acid. The method comprises: (i) amplifying, in an  
 XX isolated sample from the subject, the nucleic acid segment that, in an  
 XX affected individual contains (A), (ii) treating the amplicons with a  
 XX catalytic nucleic acid (I) that specifically recognizes and cleaves a  
 XX target sequence present in either the mutated or wild-type segments,  
 XX but not in both; and (iii) detecting any cleavage caused by (I). Step  
 XX (ii) may be performed concurrently with (i). The method is specifically  
 XX used to diagnose cancer (especially), acquired immune deficiency  
 XX syndrome and cystic fibrosis. (i) recognises as few as two bp to create  
 XX a cleavage site (contrast at least 4 bp required by enzymes used in  
 XX restriction fragment length polymorphism (RFLP) analysis); such sites  
 XX occur more frequently than restriction enzyme sites, and mismatched  
 XX primers can be used to induce cleavage sites for (I). The method is  
 XX potentially more flexible than RFLP and does not require any enzymes or  
 XX toxic compounds. AA23439 to AA234450 represent oligonucleotide  
 XX sequences used in the exemplification of the present invention.  
 XX  
 XX Sequence 29 BP; 7 A; 10 C; 5 G; 7 T; 0 other;  
 XX SQ  
 XX Query Match 97.5%; Score 15.6; DB 20; Length 29;  
 XX Best Local Similarity 93.8%; Pred. No. 35;  
 XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 RGGCTAGCTACACGA 16  
 XX :|||||  
 XX DB 9 AGGCTAGCTACACGA 24  
 XX  
 XX RESULT 15  
 XX AAC82623  
 XX ID AAC82623 standard; DNA; 29 BP.  
 XX AC AAC82623;  
 XX XX  
 XX DT 13-MAR-2001 (first entry)  
 XX XX  
 XX DE Hammerhead ribozyme DNA motif #23.  
 XX XX  
 XX KW Detection; amplification; pathogenic bacteria; hammerhead ribozyme;  
 XX fluorescent signal; cleavage; ss.  
 XX XX  
 XX OS Synthetic.  
 XX XX  
 XX PN DE19915141-A1.  
 XX XX  
 XX PD 28-SEP-2000.  
 XX XX  
 XX PF 26-MAR-1999; 99DE-1015141.  
 XX PR 26-MAR-1999; 99DE-1015141.  
 XX XX

PA (ARTU-) ARTUS GES MOLEKULARBIOLOGISCHE DIAGNOSTI.  
 XX  
 XX Krupp G;  
 XX  
 DR WPI; 2000-603196/58.  
 XX  
 PT Real-time quantitative amplification of nucleic acid, useful for  
 PT detecting bacterial pathogens, uses primer and labeled probe that  
 PT combine to form a ribozyme -  
 PS  
 XX Disclosure; Fig 13; 39pp; German.  
 XX  
 CC This invention describes a novel method for the amplification and  
 CC quantitative real-time determination of nucleic acid (I) using a primer  
 CC attached to a 1-40 nucleotide sequence (II) in the transcription product.  
 CC Amplification is done in the presence of an excess, preferably 50-500 nM,  
 CC of a nucleic acid probe (III) and labeled by a reporter molecule and a  
 CC quencher molecule. (I) encodes the motif 5'-GAA-3' (A), and (II)  
 CC contains the motif 5'-CUGAACA-3' (B). (III) has 25-60, especially 50,  
 CC nucleotides. The method is used to detect and quantify (I) from  
 CC pathogenic bacteria. The method allows real-time detection and  
 CC quantification of (I), particularly RNA by NASBA (RTM) (nucleic acid  
 CC sequence-based amplification), without the difficulties associated with  
 CC use of DNA probes (see Nucleic Acid Res., 26 (1998) 2150) and is suitable  
 CC for routine use. Specifically the combination of (A) and (B) generates a  
 CC hammerhead ribozyme that cleaves the probe and generates a fluorescent  
 CC signal. Since many probes are cleaved, a high signal is produced,  
 CC resulting in high sensitivity and shorter reaction times. The method is  
 CC very specific since exact hybridization of probe to target is necessary  
 CC for cleavage to occur. Complicated probes are not required because  
 CC cleavage results in dissociation of the probe from the target (which  
 CC allows multiplexing). Stable and inexpensive probes can be used,  
 CC consisting mainly of 2'-deoxyribonucleotides.  
 CC  
 SQ Sequence 29 BP; 5 A; 4 C; 4 G; 2 T; 14 other;  
 XX  
 Query Match 97.5%; Score 15.6; DB 21; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RGCGTAGCTACACGA 16  
 |||||  
 Db 7 RGCGTAGCTACACGA 22

RESULT 16  
 ABZ66526  
 ID ABZ66526 standard; RNA; 29 BP.  
 XX  
 AC ABZ66526;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human HER2 synthetic DNAzyme #2.  
 XX  
 KW Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US16840.  
 XX  
 PR 29-MAY-2001; 2001US-294140P.  
 PR 06-JUN-2001; 2001US-296249P.  
 PR 10-SEP-2001; 2001US-318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX

PI Mcswiggen J;  
 XX  
 DR WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
 XX  
 PS Claim 3; Page 153; 185pp; English.  
 XX  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytosolic, anti-HIV, and  
 CC anti-rheumatic activity. The nucleic acid molecules are useful for  
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
 CC acids are also useful for treating breast, ovarian, colorectal, lung,  
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ6532 - ABZ65519,  
 CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the  
 CC invention.  
 CC  
 SQ Sequence 29 BP; 11 A; 7 C; 7 G; 2 T; 2 U; 0 other;  
 XX  
 Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RGCGTAGCTACACGA 16  
 :|||  
 Db 7 RGCGTAGCTACACGA 22

RESULT 17  
 ABZ66528  
 ID ABZ66528 standard; RNA; 29 BP.  
 XX  
 AC ABZ66528;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human HER2 synthetic DNAzyme #4.  
 XX  
 KW Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US16840.  
 XX  
 PR 29-MAY-2001; 2001US-294140P.  
 PR 06-JUN-2001; 2001US-296249P.  
 PR 10-SEP-2001; 2001US-318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 P1 Mcswiggen J;  
 XX  
 DR WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
 XX  
 PS Claim 3; Page 153; 185pp; English.  
 XX  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytoskeletal, anti-HIV, and  
 CC anti-rheumatic activity. The nucleic acid molecules are useful for  
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
 CC acids are also useful for treating breast, ovarian, colorectal, lung,  
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ6532 - ABZ65519,  
 CC ABZ6525 - ABZ6529, ABZ6586 - ABZ6658 represent human ribozymes of the  
 CC invention.

CC Sequence 29 BP; 9 A; 5 C; 11 G; 2 T; 2 U; 0 other;

XX  
 SQ Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
 :|||||||  
 DB 7 AGGCTAGCTACACGA 22

RESULT 18

ABZ6529  
 ID ABZ66529 standard; RNA; 29 BP.

XX AC ABZ66529;

XX DT 21-MAR-2003 (first entry)

XX DE Human HER2 synthetic DNzyme #5.

XX KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

XX KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;  
 XX anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US16840.

XX PR 29-MAY-2001; 2001US-294140P.

XX PR 06-JUN-2001; 2001US-296249P.

XX PR 10-SEP-2001; 2001US-318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX DR WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX PS Claim 3; Page 153; 185pp; English.

XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytoskeletal, anti-HIV, and  
 CC anti-rheumatic activity. The nucleic acid molecules are useful for  
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
 CC acids are also useful for treating breast, ovarian, colorectal, lung,  
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ6532 - ABZ65519,  
 CC ABZ6525 - ABZ6529, ABZ6586 - ABZ6658 represent human ribozymes of the  
 CC invention.

XX  
 SQ Sequence 29 BP; 7 A; 4 C; 11 G; 2 T; 5 U; 0 other;

XX Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
 :|||||||  
 DB 7 AGGCTAGCTACACGA 22

RESULT 19

ABZ6649  
 ID ABZ66649 standard; RNA; 29 BP.

XX AC ABZ66649;

XX DT 21-MAR-2003 (first entry)

XX DE Human HIV enzymatic nucleic acid #1.

XX KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

XX KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;  
 XX anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US16840.

XX PR 29-MAY-2001; 2001US-294140P.

XX PR 06-JUN-2001; 2001US-296249P.

XX PR 10-SEP-2001; 2001US-318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX DR WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX PS Claim 122; Page 159; 185pp; English.

XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytoskeletal, anti-HIV, and  
 CC anti-rheumatic activity. The nucleic acid molecules are useful for  
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
 CC acids are also useful for treating breast, ovarian, colorectal, lung,  
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ6532 - ABZ65519,  
 CC ABZ6525 - ABZ6529, ABZ6586 - ABZ6658 represent human ribozymes of the  
 CC invention.

XX SQ Sequence 29 BP; 7 A; 11 C; 5 G; 2 T; 4 U; 0 other;

XX Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
 :|||||||  
 DB 7 AGGCTAGCTACACGA 22

```
RESULT 20
ABZ66650
ID ABZ66650 standard; RNA; 29 BP.
XX
XX ABZ66650;
AC
XX 21-MAR-2003 (first entry)
DT
XX Human HIV enzymatic nucleic acid #2.
DE
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
OS
XX WO200297114-A2.
PN
XX 05-DEC-2002.
PD
XX 29-MAY-2002; 2002WO-US16840.
PE
XX 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswigen J;
PI
XX WPI; 2003-140484/13.
DR
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
XX Claim 122; Page 159; 185pp; English.
PS
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.
XX
XX Sequence 29 BP; 7 A; 9 C; 5 G; 2 T; 6 U; 0 other;
SQ
Query Match 97.5%; Score 15.6; DB 25; Length 29;
Best Local Similarity 93.8%; Pred. No. 35;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGGCTAGCTACACGA 16
: |||||
DB 7 GGGCTAGCTACACGA 22
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```
RESULT 22
ABZ66652
ID ABZ66652 standard; RNA; 29 BP.
XX
XX ABZ66652;
AC
XX 21-MAR-2003 (first entry)
DT
XX Human HIV enzymatic nucleic acid #4.
DE
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
OS
XX WO200297114-A2.
PN
XX 05-DEC-2002.
PD
XX 29-MAY-2002; 2002WO-US16840.
PE
XX 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswigen J;
PI
XX WPI; 2003-140484/13.
DR
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
XX Claim 122; Page 159; 185pp; English.
PS
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.
XX
XX Sequence 29 BP; 6 A; 9 C; 6 G; 2 T; 6 U; 0 other;
SQ
Query Match 97.5%; Score 15.6; DB 25; Length 29;
Best Local Similarity 93.8%; Pred. No. 35;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGGCTAGCTACACGA 16
: |||||
DB 7 AGGCTAGCTACACGA 22
```

XX 29-MAY-2001; 2001US-294140P.  
PR 06-JUN-2001; 2001US-296249P.  
PR 10-SEP-2001; 2001US-318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswiggen J;  
XX  
XX WPI, 2003-140484/13.  
XX  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX  
XX  
PS Claim 122; Page 159; 185pp; English.  
XX  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosstatic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the  
CC invention.  
XX  
XX Sequence 29 BP; 8 A; 6 C; 8 G; 2 T; 5 U; 0 other;  
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Query Match 97.5%; Score 15.6; DB 25; Length 29;  
Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
: |||||  
DB 7 AGGCTAGCTACACGA 22

RESULT 23  
ABZ6653  
ID ABZ6653 standard; RNA; 29 BP.  
XX  
XX ABZ6653;  
AC  
XX  
XX 21-MAR-2003 (first entry)  
DT  
XX  
XX Human HIV enzymatic nucleic acid #5.  
DE  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200297114-A2.  
PN  
XX  
XX 05-DEC-2002.  
PD  
XX  
XX 29-MAY-2002; 2002WO-US16840.  
PF  
XX  
XX 29-MAY-2001; 2001US-294140P.  
PR 06-JUN-2001; 2001US-296249P.  
PR 10-SEP-2001; 2001US-318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX  
XX Mcswiggen J;  
PI  
XX  
XX WPI, 2003-140484/13.  
DR  
XX

PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -  
XX  
XX  
XX Claim 122; Page 159; 185pp; English.  
XX  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosstatic, anti-HIV, and  
CC anti-rheumatic activity. The nucleic acid molecules are useful for  
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic  
CC acids are also useful for treating breast, ovarian, colorectal, lung,  
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.  
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,  
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the  
CC invention.  
XX  
XX Sequence 29 BP; 7 A; 12 C; 5 G; 2 T; 3 U; 0 other;  
SQ

Query Match 97.5%; Score 15.6; DB 25; Length 29;  
Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
: |||||  
DB 7 AGGCTAGCTACACGA 22

RESULT 24  
ABX13988  
ID ABX13988 standard; DNA; 29 BP.  
XX  
XX ABX13988;  
AC  
XX  
XX 25-FEB-2003 (first entry)  
DT  
XX  
XX Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1594.  
DE  
XX  
XX Catalytic DNA; catalytic RNA; hairless protein; ss;  
KW hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;  
KW ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KW catalytic core; cleavage site; pharmaceutical; hair production;  
KW hair follicle; anagen phase; catagen phase; hair removal product;  
KW depilatory.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 8..22 a  
FT /\*tag= "Catalytic domain"  
FT /note= "Catalytic domain"  
XX  
XX PN WO200283891-A2.  
XX  
XX 24-OCT-2002.  
PD  
XX  
XX 12-APR-2002; 2002WO-US11683.  
PF  
XX  
XX 13-APR-2001; 2001US-283618P.  
PR  
XX  
XX (UYCO) UNIV COLUMBIA NEW YORK.  
PA  
XX  
XX Christiano AM;  
PI  
XX  
XX WPI, 2003-093020/08.  
DR  
XX  
XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
PT cell, or for inhibiting transition of a hair follicle from anagen phase  
PT to catagen phase -  
PT

XX Claim 3; Page 34; 65pp; English.

PS The invention discloses a new catalytic DNA or RNA molecule that

CC specifically cleaves, or inhibits expression of, Hairless protein mRNA

XX which comprises a catalytic domain that cleaves mRNA at a defined

CC consensus sequence and binding domains contiguous with the 5' and 3' ends

CC of the catalytic domain. Lack of expression of the hairless gene due to

CC inherited mutations leads to the complete loss of hair, known as

CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting

CC the genes promoting hair growth, and one way to get targeted, transient

CC gene suppression is through the use of catalytic nucleic acid technology,

CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have

CC a self-catalytic enzymatic function and sequence specific RNA binding

CC ability. Small DNA oligonucleotides that have a similar structure to the

CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a

CC catalytic core and two sequence specific arms. The deoxy-ribozymes have

CC more lenient consensus cleavage site requirements and are less likely to

CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids

CC are useful in pharmaceutical compositions for inhibiting hair production

CC by a hair-producing cell, for inhibiting hair growth and for inhibiting

CC the transition of a hair follicle from the anagen phase to the catagen

CC phase. A non-human transgenic mammal is useful as a model for testing

CC hair removal products which function by inhibiting hairless protein

CC expression. The sequence presented is the deoxy-ribozyme that cleaves the

CC human hairless protein mRNA immediately after nucleotide 1594.

XX

SQ Sequence 29 BP; 7 A; 10 C; 8 G; 4 T; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 29;

Best Local Similarity 93.8%; Pred. No. 35;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCTACACGA 16

Db 7 GGGCTAGCTACACGA 22

RESULT 25

ABX13989

ID ABX13989 standard; DNA; 29 BP.

XX

AC ABX13989;

XX

DT 25-FEB-2003 (first entry)

XX

DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1597.

XX

KW Catalytic DNA; catalytic RNA; hairless protein; ss;

KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;

KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;

KW catalytic core; cleavage site; pharmaceutical; hair production;

KW hair follicle; anagen phase; catagen phase; hair removal product;

KW depilatory.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT misc\_feature 8..22

FT /\*tag= a

FT /note= "Catalytic domain"

XX

XX WO200283891-A2.

XX

XX 24-OCT-2002.

XX

XX 12-APR-2002; 2002WO-US11683.

XX

XX 13-APR-2001; 2001US-283618P.

XX

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX

PI Cristiano AM;

XX

DR WPI; 2003-093020/08.

XX

PT New catalytic nucleic acid molecule that specifically cleaves Hairless

XX protein mRNA, useful for inhibiting hair production by a hair-producing

PT cell, or for inhibiting transition of a hair follicle from anagen phase

PT to catagen phase

XX

PS Claim 3; Page 34; 65pp; English.

XX

XX The invention discloses a new catalytic DNA or RNA molecule that

CC specifically cleaves, or inhibits expression of, Hairless protein mRNA

CC which comprises a catalytic domain that cleaves mRNA at a defined

CC consensus sequence and binding domains contiguous with the 5' and 3' ends

CC of the catalytic domain. Lack of expression of the hairless gene due to

CC inherited mutations leads to the complete loss of hair, known as

CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting

CC the genes promoting hair growth, and one way to get targeted, transient

CC gene suppression is through the use of catalytic nucleic acid technology,

CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have

CC a self-catalytic enzymatic function and sequence specific RNA binding

CC ability. Small DNA oligonucleotides that have a similar structure to the

CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a

CC catalytic core and two sequence specific arms. The deoxy-ribozymes have

CC more lenient consensus cleavage site requirements and are less likely to

CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids

CC are useful in pharmaceutical compositions for inhibiting hair production

CC by a hair-producing cell, for inhibiting hair growth and for inhibiting

CC the transition of a hair follicle from the anagen phase to the catagen

CC phase. A non-human transgenic mammal is useful as a model for testing

CC hair removal products which function by inhibiting hairless protein

CC expression. The sequence presented is the deoxy-ribozyme that cleaves the

CC human hairless protein mRNA immediately after nucleotide 1597.

XX

SQ Sequence 29 BP; 7 A; 9 C; 10 G; 3 T; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 29;

Best Local Similarity 93.8%; Pred. No. 35;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCTACACGA 16

Db 7 AGGCTAGCTACACGA 22

RESULT 26

ABX13990

ID ABX13990 standard; DNA; 29 BP.

XX

AC ABX13990;

XX

DT 25-FEB-2003 (first entry)

XX

DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1641.

XX

KW Catalytic DNA; catalytic RNA; hairless protein; ss;

KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;

KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;

KW catalytic core; cleavage site; pharmaceutical; hair production;

KW hair follicle; anagen phase; catagen phase; hair removal product;

KW depilatory.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT misc\_feature 8..22

FT /\*tag= a

FT /note= "Catalytic domain"

XX

XX WO200283891-A2.

XX

PD 24-OCT-2002.  
 XX  
 XX 12-APR-2002; 2002WO-US11683.  
 PF  
 XX 13-APR-2001; 2001US-283618P.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX Cristiano AM;  
 PI  
 XX WPI; 2003-093020/08.  
 DR  
 XX  
 XX  
 PT New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase  
 PS  
 XX Claim 3; Page 34; 65pp; English.  
 CC The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 1641.  
 CC  
 XX  
 SQ Sequence 29 BP; 7 A; 11 C; 7 G; 4 T; 0 other;  
 QY  
 Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 RGGCTAGCTACACGA 16  
 7 AGGCTAGCTACACGA 22  
 RESULT 27  
 ABX13991 standard; DNA; 29 BP.  
 XX  
 XX ABX13991;  
 AC  
 XX 25-FEB-2003 (first entry)  
 DT  
 XX  
 XX Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1698.  
 DE  
 XX Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
 KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
 KW catalytic core; cleavage site; pharmaceutical; hair production;  
 KW hair follicle; anagen phase; catagen phase; hair removal product;  
 KW depilatory.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 8..22  
 FT /tag= a  
 FT /note= "Catalytic domain"  
 FT  
 XX WO200283991-A2.  
 XX  
 XX 24-OCT-2002.  
 PD  
 XX  
 XX  
 PF 12-APR-2002; 2002WO-US11683.  
 XX  
 XX 13-APR-2001; 2001US-283618P.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX Cristiano AM;  
 PI  
 XX WPI; 2003-093020/08.  
 DR  
 XX  
 XX  
 PT New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase  
 PS  
 XX Claim 3; Page 34; 65pp; English.  
 CC The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 1698.  
 CC  
 XX  
 SQ Sequence 29 BP; 7 A; 7 C; 10 G; 5 T; 0 other;  
 QY  
 Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 RGGCTAGCTACACGA 16  
 7 AGGCTAGCTACACGA 22  
 RESULT 28  
 ABX13992 standard; DNA; 29 BP.  
 XX  
 XX ABX13992;  
 AC  
 XX 25-FEB-2003 (first entry)  
 DT  
 XX  
 XX Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1732.  
 DE  
 XX Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KW

KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KW catalytic core; cleavage site; pharmaceutical; hair production;  
KW hair follicle; anagen phase; catagen phase; hair removal product;  
KW depilatory.  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 8..22  
FT /\*tag= a  
FT /note= "Catalytic domain"  
XX  
XX WO200283891-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 12-APR-2002; 2002WO-US11683.  
XX  
XX 13-APR-2001; 2001US-283618P.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX Christiano AM;  
XX  
XX WPI; 2003-093020/08.  
XX  
XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
XX Protein mRNA, useful for inhibiting hair production by a hair-producing  
XX cell, or for inhibiting transition of a hair follicle from anagen phase  
XX to catagen phase -  
XX  
XX Claim 3; Page 34; 65pp; English.  
XX  
XX The invention discloses a new catalytic DNA or RNA molecule that  
XX specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
XX which comprises a catalytic domain that cleaves mRNA at a defined  
XX consensus sequence and binding domains contiguous with the 5' and 3' ends  
XX of the catalytic domain. Lack of expression of the hairless gene due to  
XX inherited mutations leads to the complete loss of hair, known as  
XX atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
XX the genes promoting hair growth, and one way to get targeted, transient  
XX gene suppression is through the use of catalytic nucleic acid technology,  
XX including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
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XX hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
XX catalytic core and two sequence specific arms. The deoxy-ribozymes have  
XX more lenient consensus cleavage site requirements and are less likely to  
XX degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
XX are useful in pharmaceutical compositions for inhibiting hair production  
XX by a hair-producing cell, for inhibiting hair growth and for inhibiting  
XX the transition of a hair follicle from the anagen phase to the catagen  
XX phase. A non-human transgenic mammal is useful as a model for testing  
XX hair removal products which function by inhibiting hairless protein  
XX expression. The sequence presented is the deoxy-ribozyme that cleaves the  
XX human hairless protein mRNA immediately after nucleotide 1732.  
XX  
SQ Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;  
Query Match 97.5%; Score 15.6; DB 25; Length 29;  
Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCTACACGA 16  
Db 7 AGGCTAGCTACACGA 22

RESULT 29  
ABX13993  
ID ABX13993 standard; DNA; 29 BP.

XX  
AC ABX13993;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
XX Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1750.  
XX  
XX Catalytic DNA; catalytic RNA; hairless protein; ss;  
KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KW catalytic core; cleavage site; pharmaceutical; hair production;  
KW hair follicle; anagen phase; catagen phase; hair removal product;  
KW depilatory.  
XX  
XX Homo sapiens.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
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XX misc\_feature 8..22  
XX /\*tag= a  
XX /note= "Catalytic domain"  
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XX WO200283891-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 12-APR-2002; 2002WO-US11683.  
XX  
XX 13-APR-2001; 2001US-283618P.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX Christiano AM;  
XX  
XX WPI; 2003-093020/08.  
XX  
XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
XX Protein mRNA, useful for inhibiting hair production by a hair-producing  
XX cell, or for inhibiting transition of a hair follicle from anagen phase  
XX to catagen phase -  
XX  
XX Claim 3; Page 34; 65pp; English.  
XX  
XX The invention discloses a new catalytic DNA or RNA molecule that  
XX specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
XX which comprises a catalytic domain that cleaves mRNA at a defined  
XX consensus sequence and binding domains contiguous with the 5' and 3' ends  
XX of the catalytic domain. Lack of expression of the hairless gene due to  
XX inherited mutations leads to the complete loss of hair, known as  
XX atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
XX the genes promoting hair growth, and one way to get targeted, transient  
XX gene suppression is through the use of catalytic nucleic acid technology,  
XX including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
XX a self-catalytic enzymatic function and sequence specific RNA binding  
XX ability. Small DNA oligonucleotides that have a similar structure to the  
XX hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
XX catalytic core and two sequence specific arms. The deoxy-ribozymes have  
XX more lenient consensus cleavage site requirements and are less likely to  
XX degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
XX are useful in pharmaceutical compositions for inhibiting hair production  
XX by a hair-producing cell, for inhibiting hair growth and for inhibiting  
XX the transition of a hair follicle from the anagen phase to the catagen  
XX phase. A non-human transgenic mammal is useful as a model for testing  
XX hair removal products which function by inhibiting hairless protein  
XX expression. The sequence presented is the deoxy-ribozyme that cleaves the  
XX human hairless protein mRNA immediately after nucleotide 1750.  
XX  
SQ Sequence 29 BP; 8 A; 9 C; 7 G; 5 T; 0 other;  
Query Match 97.5%; Score 15.6; DB 25; Length 29;  
Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy	I	RCGCTACTACAAGA	16
	:		
	:		
Db	7	GCGCTACTACAAGA	22
	RESULT	30	
ID	ABX13994		
AC	ABX13994 standard; DNA; 29 BP.		
XX	ABX13994;		
DT	25-FEB-2003 (first entry)		
XX			
DE	Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1801.		
XX			
KW	Catalytic DNA; catalytic RNA; hairless protein; ss;		
KW	hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;		
KW	ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;		
KW	catalytic core; cleavage site; pharmaceutical; hair production;		
KW	hair follicle; anagen phase; catagen phase; hair removal product;		
KW	deplatory.		
XX			
OS	Homo sapiens.		
XX	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	misc_feature	8..22	
FT		/tag= a	
FT		/note= "Catalytic domain"	
XX			
PN	WO200283891-A2.		
PD	24-OCT-2002.		
XX			
PF	12-APR-2002; 2002WO-US11683.		
XX			
PR	13-APR-2001; 2001US-283618P.		
PA	(UYCO ) UNIV COLUMBIA NEW YORK.		
PI	Christiano AM;		
DR	WPI; 2003-093020/08.		
XX			
PT	New catalytic nucleic acid molecule that specifically cleaves Hairless Protein mRNA, useful for inhibiting hair production by a hair-producing cell, or for inhibiting transition of a hair follicle from anagen phase to catagen phase -		
PT			
PS	Claim 3; Page 34; 65pp; English.		
XX			
XX	The invention discloses a new catalytic DNA or RNA molecule that specifically cleaves, or inhibits expression of, Hairless Protein RNA which comprises a catalytic domain that cleaves mRNA at a defined consensus sequence and binding domains contiguous with the 5' and 3' ends of the catalytic domain. Lack of expression of the hairless gene due to inherited mutations leads to the complete loss of hair, known as atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting the genes promoting hair growth, and one way to get targeted, transient gene suppression is through the use of catalytic nucleic acid technology, including ribozymes and DNazymes. Ribozymes are RNA structures which have a self-catalytic enzymatic function and sequence specific RNA binding ability. Small DNA oligonucleotides that have a similar structure to the hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a catalytic core and two sequence specific arms. The deoxy-ribozymes have more lenient consensus cleavage site requirements and are less likely to degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids are useful in pharmaceutical compositions for inhibiting hair production by a hair-producing cell, for inhibiting hair growth and for inhibiting the transition of a hair follicle from the anagen phase to the catagen phase. A non-human transgenic mammal is useful as a model for testing hair removal products which function by inhibiting hairless protein expression. The sequence presented is the deoxy-ribozyme that cleaves the		

CC human hairless protein mRNA immediately after nucleotide 1801.  
SQ Sequence 29 BP; 9 A; 6 C; 11 G; 3 T; 0 other;  
Query Match 97.5%; Score 15.6; DB 25; Length 29;  
Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
          :|||||  
DB 7 AGGCTAGCTACACGA 22

RESULT 21  
ABX13995  
ID ABX13995 standard; DNA; 29 BP.  
XX  
XX AC ABX13995;  
XX  
DT 25-FEB-2003 (first entry)  
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1811.  
XX  
XX  
XX Catalytic DNA; catalytic RNA; hairless protein; ss;  
KW hair loss; arrichia; hair growth; hirsutism; catalytic nucleic acid;  
KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KW catalytic core; cleavage site; pharmaceutical; hair production;  
KW hair follicle; anagen phase; catagen phase; hair removal product;  
KW depilatory.  
XX  
XX Homo sapiens.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT misc\_feature 8..22  
FT /\*tag= a /note= "Catalytic domain"  
FT  
XX MO200283891-A2.  
PN  
PD 24-OCT-2002.  
XX  
PF 12-APR-2002; 2002MO-US11683.  
PR 13-APR-2001; 2001US-283618P.  
PA (UWCO ) UNIV COLUMBIA NEW YORK.  
PI Christiano AM;  
DR WPI; 2003-093020/08.  
XX  
XX  
PT New catalytic nucleic acid molecule that specifically cleaves Hairless  
PT protein mRNA, useful for inhibiting hair production by a hair-producing  
PT cell, or for inhibiting transition of a hair follicle from anagen phase  
PT to catagen phase -  
PS Claim 3; Page 35; 65pp; English.

The invention discloses a new catalytic DNA or RNA molecule that specifically cleaves, or inhibits expression of, Hairless protein mRNA which comprises a catalytic domain that cleaves mRNA at a defined consensus sequence and binding domains contiguous with the 5' and 3' ends of the catalytic domain. Lack of expression of the hairless gene due to inherited mutations leads to the complete loss of hair, known as atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting the genes promoting hair growth, and one way to get targeted, transient gene suppression is through the use of catalytic nucleic acid technology, including ribozymes and DNazymes. Ribozymes are RNA structures which have a self-catalytic enzymatic function and sequence specific RNA binding ability. Small DNA oligonucleotides that have a similar structure to the hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a catalytic core and two sequence specific arms. The deoxy-ribozymes have

CC more lentient consensus cleavage site requirements and are less likely to  
CC degrade, in vivo, that hammerhead ribozymes. The catalytic nucleic acids  
CC are useful in pharmaceutical compositions for inhibiting hair production  
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
CC the transition of a hair follicle from the anagen phase to the catagen  
CC phase. A non-human transgenic mammal is useful as a model for testing  
CC hair removal products which function by inhibiting hairless protein  
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
CC human hairless protein mRNA immediately after nucleotide 1811.  
XX  
SQ Sequence 29 BP; 9 A; 9 C; 9 G; 2 T; 0 other;  
Qy  
Query Match 97.5%; Score 15.6; DB 25; Length 29;  
Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 RGGCTAGCTACACGA 16  
7 AGGCTAGCTACACGA 22  
Db  
RESULT 32  
ABX13996  
ID ABX13996 standard; DNA; 29 BP.  
XX  
AC ABX13996;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2028.  
XX  
KM Catalytic DNA; catalytic RNA; hairless protein; ss;  
KM hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;  
KM ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KM catalytic core; cleavage site; pharmaceutical; hair production;  
KM hair follicle; anagen phase; catagen phase; hair removal product;  
KM depilatory.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 8..22  
FT /\*tag= a  
FT /note= "Catalytic domain"  
FT  
FT  
PN WO200283891-A2.  
XX  
PD 24-OCT-2002.  
XX  
PP 12-APR-2002; 2002WO-US11683.  
XX  
PR 13-APR-2001; 2001US-283618P.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Christiano AM;  
XX  
DR WPI; 2003-093020/08.  
XX  
PT New catalytic nucleic acid molecule that specifically cleaves Hairless  
PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
PT cell, or for inhibiting transition of a hair follicle from anagen phase  
PT to catagen phase -  
XX  
PS Claim 3; Page 35; 65pp; English.  
XX  
CC The invention discloses a new catalytic DNA or RNA molecule that  
CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
CC which comprises a catalytic domain that cleaves mRNA at a defined  
CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
CC of the catalytic domain. Lack of expression of the hairless gene due to  
CC inherited mutations leads to the complete loss of hair, known as

CC atichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
CC the genes promoting hair growth, and one way to get targeted, transient  
CC gene suppression is through the use of catalytic nucleic acid technology,  
CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
CC a self-catalytic enzymatic function and sequence specific RNA binding  
CC ability. Small DNA oligonucleotides that have a similar structure to the  
CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
CC more lentient consensus cleavage site requirements and are less likely to  
CC degrade, in vivo, that hammerhead ribozymes. The catalytic nucleic acids  
CC are useful in pharmaceutical compositions for inhibiting hair production  
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
CC the transition of a hair follicle from the anagen phase to the catagen  
CC phase. A non-human transgenic mammal is useful as a model for testing  
CC hair removal products which function by inhibiting hairless protein  
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
CC human hairless protein mRNA immediately after nucleotide 2028.  
XX  
SQ Sequence 29 BP; 6 A; 7 C; 13 G; 3 T; 0 other;  
Qy  
Query Match 97.5%; Score 15.6; DB 25; Length 29;  
Best Local Similarity 93.8%; Pred. No. 35;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 RGGCTAGCTACACGA 16  
7 GGCTAGCTACACGA 22  
Db  
RESULT 33  
ABX13997  
ID ABX13997 standard; DNA; 29 BP.  
XX  
AC ABX13997;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2033.  
XX  
KM Catalytic DNA; catalytic RNA; hairless protein; ss;  
KM hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;  
KM ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
KM catalytic core; cleavage site; pharmaceutical; hair production;  
KM hair follicle; anagen phase; catagen phase; hair removal product;  
KM depilatory.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 8..22  
FT /\*tag= a  
FT /note= "Catalytic domain"  
FT  
FT  
PN WO200283891-A2.  
XX  
PD 24-OCT-2002.  
XX  
PP 12-APR-2002; 2002WO-US11683.  
XX  
PR 13-APR-2001; 2001US-283618P.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Christiano AM;  
XX  
DR WPI; 2003-093020/08.  
XX  
PT New catalytic nucleic acid molecule that specifically cleaves Hairless  
PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
PT cell, or for inhibiting transition of a hair follicle from anagen phase  
PT to catagen phase -  
XX



XX 12-APR-2002; 2002WO-US11683.  
 PR 13-APR-2001; 2001US-283618P.  
 PR (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Christiano AM;  
 PI WPI; 2003-093020/08.  
 DR New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase -  
 XX  
 XX Claim 3; Page 35; 65pp; English.  
 PS  
 XX The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 2083.  
 XX  
 SQ Sequence 29 BP; 9 A; 7 C; 9 G; 4 T; 0 other;  
 Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGCTAGCTACACGA 16  
 :|||||||  
 Db 7 GGCTAGCTACACGA 22  
 :|||||||  
 RESULT 36  
 ABX14001 standard; DNA; 29 BP.  
 ID ABX14001;  
 AC ABX14001;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2380.  
 XX  
 KM Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;  
 KM ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
 KM catalytic core; cleavage site; pharmaceutical; hair production;  
 KM hair follicle; anagen phase; catagen phase; hair removal product;  
 KM depilatory.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 XX

PH Key Location/Qualifiers  
 FT misc\_feature 8..22  
 FT /\*tag= a  
 FT /note= "Catalytic domain"  
 PN WO200283691-A2.  
 XX  
 XX 24-OCT-2002.  
 PD  
 XX  
 XX 12-APR-2002; 2002WO-US11683.  
 PR 13-APR-2001; 2001US-283618P.  
 PR (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Christiano AM;  
 PI WPI; 2003-093020/08.  
 DR  
 XX  
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing  
 PT cell, or for inhibiting transition of a hair follicle from anagen phase  
 PT to catagen phase -  
 XX  
 XX Claim 3; Page 35; 65pp; English.  
 PS  
 XX The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 2380.  
 XX  
 SQ Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;  
 Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGCTAGCTACACGA 16  
 :|||||||  
 Db 7 AGCTAGCTACACGA 22  
 :|||||||  
 RESULT 37  
 ABX14002 standard; DNA; 29 BP.  
 ID ABX14002;  
 AC ABX14002;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2395.  
 XX  
 KM Catalytic DNA; catalytic RNA; hairless protein; ss;  
 KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;

KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;  
 KW catalytic core; cleavage site; pharmaceutical; hair production;  
 KW hair follicle; anagen phase; catagen phase; hair removal product;  
 KW deplatory.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FT Key location/Qualifiers  
 FT misc\_feature 8..22  
 FT /tag= a  
 FT /note= "Catalytic domain"  
 XX  
 XX MO200283891-A2.  
 XX  
 XX 24-OCT-2002.  
 XX  
 XX 12-APR-2002; 2002WO-US11683.  
 XX  
 XX 13-APR-2001; 2001US-283618P.  
 XX  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 XX Cristiano AM;  
 XX  
 XX WPI; 2003-093020/08.  
 XX  
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless  
 XX Protein mRNA, useful for inhibiting hair production by a hair-producing  
 XX cell, or for inhibiting transition of a hair follicle from anagen phase  
 XX to catagen phase  
 XX  
 PS Claim 3; Page 35; 65pp; English.  
 XX  
 CC The invention discloses a new catalytic DNA or RNA molecule that  
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA  
 CC which comprises a catalytic domain that cleaves mRNA at a defined  
 CC consensus sequence and binding domain contiguous with the 5' and 3' ends  
 CC of the catalytic domain. Lack of expression of the hairless gene due to  
 CC inherited mutations leads to the complete loss of hair, known as  
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting  
 CC the genes promoting hair growth, and one way to get targeted, transient  
 CC gene suppression is through the use of catalytic nucleic acid technology,  
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have  
 CC a self-catalytic enzymatic function and sequence specific RNA binding  
 CC ability. Small DNA oligonucleotides that have a similar structure to the  
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a  
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have  
 CC more lenient consensus cleavage site requirements and are less likely to  
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids  
 CC are useful in pharmaceutical compositions for inhibiting hair production  
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting  
 CC the transition of a hair follicle from the anagen phase to the catagen  
 CC phase. A non-human transgenic mammal is useful as a model for testing  
 CC hair removal products which function by inhibiting hairless protein  
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the  
 CC human hairless protein mRNA immediately after nucleotide 2395.  
 CC  
 XX  
 SQ Sequence 29 BP; 9 A; 9 C; 8 G; 3 T; 0 other;  
 XX  
 Query Match 97.5%; Score 15.6; DB 25; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGGCTAGCTTACACGA 16  
 :|||||  
 DB 7 GGGCTAGCTTACACGA 22  
 RESULT 38  
 AA14525/C  
 ID AA14525 standard; DNA; 30 BP.  
 XX

AC AA14525;  
 XX  
 XX 08-AUG-2000 (first entry)  
 DT  
 XX  
 DE Oligonucleotide 5'-polynm-gaglink-(Pleio)-DNase-1023-B/P.  
 XX  
 XX Reverse transcriptase; RNase H; stem-loop structure; genetic element;  
 KW inverted tandem repeat; vector; inhibitory nucleic acid;  
 KW antisense sequence; aptamer; gene expression; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200022114-A1.  
 EN  
 XX 20-APR-2000.  
 XX  
 XX 12-OCT-1999; 99WO-US23936.  
 XX  
 XX 09-OCT-1998; 98US-0169793.  
 XX  
 XX 16-SEP-1999; 99US-0397782.  
 PR  
 XX 04-OCT-1999; 99US-0169793.  
 XX  
 XX (INGE-) INGENE INC.  
 PA  
 XX  
 XX Conrad CA;  
 FI  
 XX  
 XX WPI; 2000-317974/27.  
 DR  
 XX  
 XX Genetic element for producing and delivering single-stranded DNA,  
 PT comprises a gene encoding reverse transcriptase and a sequence of  
 PT interest flanked by an inverted tandem repeat and primer binding site  
 PT  
 PT  
 PS Disclosure; Page 45; 77pp; English.  
 XX  
 CC The specification describes methods for producing single-stranded cDNA  
 CC (ssCDNA) in eukaryotic cells. They use a DNA cassette that produces  
 CC ssCDNA in vivo. The cassette contains the Moloney murine leukemia virus  
 CC reverse transcriptase/RNase H, a bacterial restriction endonuclease  
 CC gene, and a sequence of interest which produces a RNA template from  
 CC which the reverse transcriptase synthesizes cDNA of a specified sequence.  
 CC The ssCDNA is then modified to remove all flanking vector sequences by  
 CC taking advantage of the stem-loop structure of the cDNA, which forms as  
 CC a result of the inclusion of a inverted tandem repeat that allows the  
 CC ssCDNA to fold back on itself, forming a double stranded DNA stem, in  
 CC the sequence of interest. The double-stranded stem contains one or more  
 CC functional genetic elements (GE), adapted for incorporation into a vector  
 CC for delivery to a cell. The vectors are is useful for producing a ssDNA  
 CC sequence of interest, particularly a cDNA transcript, an inhibitory  
 CC nucleic acid molecule which is an antisense sequence or aptamer, an mRNA  
 CC transcript and a heteroduplex molecule. Inhibitory nucleic acid molecules  
 CC to a target cell are useful for alleviating pathological conditions by  
 CC regulating gene expression. The present oligonucleotide was used to  
 CC produce a vector for use in the course of the invention.  
 CC  
 XX  
 SQ Sequence 30 BP; 5 A; 8 C; 8 G; 9 T; 0 other;  
 XX  
 Query Match 97.5%; Score 15.6; DB 21; Length 30;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGGCTAGCTTACACGA 16  
 :|||||  
 DB 24 AGGCTAGCTTACACGA 9  
 RESULT 39  
 AA287648  
 ID AA287648 standard; DNA; 30 BP.  
 XX  
 XX AA287648;  
 AC  
 XX 09-MAY-2000 (first entry)  
 DT

XX Human short protein kinase C (PKC)alpha DNA ribozyme.  
 DE Ribozyme; hammerhead; RNase degradation; catalytic; PKCalpha; VEGF;  
 XX protein kinase C alpha; tumour necrosis factor alpha; TNFalpha; cancer;  
 KW vascular epithelial growth factor; gene expression; malignant glioma;  
 KM cell proliferation; cytostatic; human; ss.  
 XX Homo sapiens.  
 OS  
 XX MO9963066-A2.  
 PN  
 XX 09-DEC-1999.  
 PD  
 XX 28-MAY-1999; 99WO-GB01706.  
 PF  
 XX 01-JUN-1998; 98GB-0011750.  
 PR  
 XX (NORA-) NORMEGIAN RADIIUM HOSPITAL RES FOUND.  
 PA (DZIE/) DZIEGLAWSKA H E.  
 XX  
 PI Sloud M;  
 XX  
 DR WPI; 2000-147046/13.  
 XX  
 PT Novel ribozymes, used for inhibiting the proliferation of cells, e.g.  
 PT for treating or preventing cancers -  
 PS Disclosure; Page 9; 93pp; English.  
 XX  
 CC The invention provides novel modified ribozymes that have 3 or more  
 CC pyrimidine nucleotides (PMN) in the ribozyme modified at the 2'-position,  
 CC where the PMNs are modified to 2'-amino PMNs and the ribozymes exhibit  
 CC improved stability to RNase degradation and exhibits 85% or more  
 CC catalytic activity of the unmodified ribozymes. The ribozymes of the  
 CC invention are selected from rat and human protein kinase C (PKC)alpha  
 CC ribozymes, tumour necrosis factor (TNF)alpha ribozyme, rat and human  
 CC vascular epithelial growth factor (VEGF) ribozymes. These ribozymes can  
 CC be used for treating or preventing a disease or condition responsive to  
 CC an alteration in the expression of a gene, where the ribozyme is capable  
 CC of cleaving the RNA transcribed from the gene. They can be used for  
 CC treating or preventing a disease or condition associated with the  
 CC proliferation of rapidly dividing cells, e.g. cancer such as malignant  
 CC glioma. They can also be used for inhibiting the proliferation of cells.  
 CC The use of 2'-amino modified pyrimidine can provide ribozymes of improved  
 CC stability which retain the activity of the unmodified ribozyme. The  
 CC present sequence represents a human short PKCalpha DNA ribozyme.  
 CC  
 XX  
 SQ Sequence 30 BP; 7 A; 11 C; 8 G; 4 T; 0 other;  
 QY  
 Query Match 97.5%; Score 15.6; DB 21; Length 30;  
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 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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 8 AGGCTAGCTACACGA 23  
 RESULT 40  
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 ID AAS02302 standard; cDNA; 30 BP.  
 XX  
 AC AAS02302;  
 XX  
 DT 18-JUN-2001 (first entry)  
 XX  
 DE Synthetic oligodeoxynucleotide 5'-polyNM-gaglink-(Pleio)-DNase-1023-B/P.  
 XX  
 KW ODN, oligodeoxynucleotide; inverted tandem repeat; primer binding site;  
 KW stem-loop; c-myc; viral gene; gene therapy; reverse transcription; ss;  
 KW endogenous target nucleic acid; gene inactivation; RNA splicing;  
 KW site-directed mutagenesis; cellular function interruption;

KW nucleic acid duplex binding; nucleic acid triplex binding.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200125419-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PP 04-OCT-2000; 2000WO-US27381.  
 XX  
 PR 04-OCT-1999; 99US-0411568.  
 PR 28-FEB-2000; 2000US-0514707.  
 XX  
 PA (CYTO-) CYTOGENIX INC.  
 XX  
 PI Conrad CA, Chen Y;  
 XX  
 DR WPI; 2001-266304/27.  
 XX  
 PT Alteration of expression of an endogenous nucleic acid for use in gene  
 PT therapy comprises the expression of a specific antisense sequence -  
 PS Disclosure; Page 43; 61pp; English.  
 XX  
 CC The sequence represents a synthetic single stranded cDNA. This DNA exists  
 CC in a target cell and is transfected with a cassette comprising a sequence  
 CC of interest flanked by inverted tandem repeats (ITR) and a primer binding  
 CC site (PBS) 3' to the tandem repeat. Transcription of the cassette by the  
 CC target cell produces an RNA template which is reverse transcribed to  
 CC produce ss-cDNA of a specified sequence. The ss-cDNA folds back on itself  
 CC as a result of the inverted tandem repeat, to form a stem-loop structure.  
 CC The loop is comprised of the sequence of interest. The cDNA transcript is  
 CC bound to an endogenous nucleic acid target to alter expression of the  
 CC target sequence. This method is useful for altering the expression of  
 CC gene products e.g. c-myc or a viral gene product. It may be applied to  
 CC gene therapy, with target genes mutated or introduced for therapeutic  
 CC purposes, such as gene inactivation using duplex or triplex binding of  
 CC nucleic acids, site-directed mutagenesis, interruption of cellular  
 CC function by binding to specific cellular proteins and interfering with  
 CC RNA splicing functions.  
 CC  
 XX  
 SQ Sequence 30 BP; 5 A; 8 C; 8 G; 9 T; 0 other;  
 QY  
 Query Match 97.5%; Score 15.6; DB 22; Length 30;  
 Best Local Similarity 93.8%; Pred. No. 35;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 RGGCTAGCTACACGA 16  
 24 AGGCTAGCTACACGA 9  
 Search completed: January 21, 2004, 06:52:48  
 Job time : 156.5 secs

4-29-98

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:45:02 ; Search time 38 Seconds  
(without alignments)  
185.846 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16

Sequence: 1 rgcgtagctacacga 16

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 830498

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA: \*  
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5: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	15.6	97.5	16	4	US-09-536-393-20
3	15.6	97.5	29	4	US-09-270-140A-23
4	15.6	97.5	29	4	US-09-270-140A-25
5	15.6	97.5	30	4	US-09-270-140A-55
6	15.6	97.5	31	3	US-09-253-955-5
7	15.6	97.5	31	3	US-09-637-405-5
8	15.6	97.5	31	4	US-09-270-140A-42
9	15.6	97.5	31	4	US-09-270-140A-45
10	15.6	97.5	31	4	US-09-270-140A-48
11	15.6	97.5	31	4	US-09-270-140A-51
12	15.6	97.5	31	4	US-09-746-985B-5
13	15.6	97.5	32	4	US-09-270-140A-12
14	15.6	97.5	32	4	US-09-270-140A-15
15	15.6	97.5	32	4	US-09-270-140A-19
16	15.6	97.5	32	4	US-09-270-140A-28
17	15.6	97.5	32	4	US-09-270-140A-58
18	15.6	97.5	34	4	US-09-270-140A-9
19	15.6	97.5	34	4	US-09-270-140A-53
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21	15.6	97.5	35	4	US-09-270-140A-6
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23	15.6	97.5	35	4	US-09-270-140A-39
24	15.6	97.5	38	4	US-09-270-140A-34
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30	15.6	97.5	49	4	US-08-849-567A-81	Sequence 81, Appl
31	15.6	97.5	50	3	US-09-253-955-8	Sequence 8, Appl
32	15.6	97.5	50	3	US-09-637-405-8	Sequence 8, Appl
33	15.6	97.5	50	3	US-09-746-985B-8	Sequence 8, Appl
34	15.6	97.5	51	4	US-08-849-567A-86	Sequence 86, Appl
35	15.6	97.5	59	3	US-09-253-955-2	Sequence 2, Appl
36	15.6	97.5	59	3	US-09-637-405-2	Sequence 2, Appl
37	15.6	97.5	60	3	US-09-746-985B-2	Sequence 2, Appl
38	15.6	97.5	60	3	US-09-253-955-10	Sequence 10, Appl
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52	12	75.0	40	3	US-08-404-796-83	Sequence 83, Appl
53	12	75.0	40	3	US-08-931-869-83	Sequence 83, Appl
54	12	75.0	40	4	US-09-350-399-83	Sequence 83, Appl
55	12	75.0	40	4	US-09-236-140A-83	Sequence 83, Appl
56	11.8	73.8	75	4	US-09-702-705-242	Sequence 242, App
57	11.8	73.8	75	4	US-09-736-457-242	Sequence 242, App
58	11.8	73.8	78	4	US-09-702-705-1277	Sequence 1277, Ap
59	11.4	71.2	24	3	US-08-940-968-14	Sequence 14, Appl
60	11.4	71.2	27	4	US-09-109-329-26	Sequence 26, Appl
61	11.4	71.2	27	4	US-08-729-601A-18	Sequence 18, Appl
62	11.4	71.2	20	1	US-08-303-270-9	Sequence 9, Appl
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64	10.8	67.5	17	1	US-08-385-388-15	Sequence 15, Appl
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67	10.8	67.5	17	4	US-09-166-205B-15	Sequence 15, Appl
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76	10.8	67.5	26	2	US-08-635-761-19	Sequence 19, Appl
77	10.8	67.5	26	2	US-08-635-761-20	Sequence 20, Appl
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79	10.8	67.5	26	3	US-09-312-520-18	Sequence 18, Appl
80	10.8	67.5	26	3	US-09-312-520-19	Sequence 19, Appl
81	10.8	67.5	26	3	US-09-312-520-20	Sequence 20, Appl
82	10.8	67.5	27	3	US-08-981-189B-18	Sequence 18, Appl
83	10.8	67.5	30	3	US-08-242-197-5	Sequence 5, Appl
84	10.8	67.5	30	3	US-09-242-197-7	Sequence 7, Appl
85	10.8	67.5	32	1	US-07-977-696C-8	Sequence 8, Appl
86	10.8	67.5	32	1	US-08-129-930B-8	Sequence 8, Appl
87	10.8	67.5	32	1	US-08-976-388A-8	Sequence 8, Appl
88	10.8	67.5	35	1	US-08-551-459-8	Sequence 8, Appl
89	10.8	67.5	35	4	US-09-085-120-15	Sequence 15, Appl
90	10.8	67.5	41	3	US-08-997-918-36	Sequence 36, Appl
91	10.8	67.5	42	3	US-09-079-984A-5	Sequence 5, Appl
92	10.8	67.5	42	3	US-09-390-729-5	Sequence 5, Appl
93	10.8	67.5	44	3	US-09-254-023B-7	Sequence 7, Appl
94	10.8	67.5	44	3	US-09-350-237-25	Sequence 25, Appl
95	10.8	67.5	45	3	US-09-315-794-4	Sequence 4, Appl
96	10.8	67.5	45	3	US-09-389-341-4	Sequence 4, Appl
97	10.8	67.5	48	3	US-08-997-918-43	Sequence 43, Appl
98	10.8	67.5	50	1	US-08-519-197-5	Sequence 5, Appl
99	10.8	67.5	50	1	US-08-997-918-41	Sequence 41, Appl
100	10.8	67.5	50	3	US-08-997-918-41	Sequence 41, Appl

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102	10.8	67.5	50	3	US-09-292-071-4	Sequence 3, Appl1	175	10.4	65.0	55	2	US-08-811-492-135	Sequence 125, App
103	10.8	67.5	50	3	US-09-292-069A-3	Sequence 3, Appl1	176	10.4	65.0	55	2	US-08-475-458-10	Sequence 10, Appl1
104	10.8	67.5	50	3	US-09-292-069A-4	Sequence 3, Appl1	177	10.4	65.0	55	2	US-08-475-458-11	Sequence 10, Appl1
105	10.8	67.5	50	3	US-09-418-721-3	Sequence 3, Appl1	178	10.4	65.0	55	3	US-08-980-400-10	Sequence 10, Appl1
106	10.8	67.5	50	3	US-09-418-721-4	Sequence 3, Appl1	179	10.4	65.0	55	3	US-08-980-400-11	Sequence 10, Appl1
107	10.8	67.5	50	4	US-09-767-013-3	Sequence 3, Appl1	180	10.4	65.0	55	3	US-09-583-459A-10	Sequence 10, Appl1
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109	10.8	67.5	50	4	US-09-292-072-3	Sequence 3, Appl1	182	10.4	65.0	55	3	US-09-583-459A-10	Sequence 10, Appl1
110	10.8	67.5	50	4	US-09-292-072-4	Sequence 3, Appl1	183	10.4	65.0	55	3	US-09-583-459A-11	Sequence 10, Appl1
111	10.8	67.5	50	4	US-09-170-496D-237	Sequence 238, App	184	10.4	65.0	55	4	US-09-583-459A-10	Sequence 10, Appl1
112	10.8	67.5	50	4	US-09-170-496D-238	Sequence 238, App	185	10.4	65.0	55	4	US-09-583-459A-11	Sequence 10, Appl1
113	10.8	67.5	50	3	US-08-997-918-48	Sequence 37, Appl1	186	10.4	65.0	55	4	US-09-435-055-11	Sequence 11, Appl1
114	10.8	67.5	50	3	US-08-290-736C-37	Sequence 67, Appl1	187	10.4	65.0	55	4	US-09-011-338-65	Sequence 87, Appl1
115	10.8	67.5	71	2	US-08-465-591A-67	Sequence 252, App	188	10.4	65.0	55	4	US-08-219-012-87	Sequence 275, App
116	10.8	67.5	71	2	US-08-465-591A-67	Sequence 252, App	189	10.4	65.0	75	3	US-08-687-421-275	Sequence 16, Appl1
117	10.8	67.5	71	2	US-08-973-124-252	Sequence 46, Appl1	190	10.4	63.7	33	1	US-07-979-962A-16	Sequence 44, Appl1
118	10.8	67.5	71	3	US-08-290-736C-46	Sequence 252, App	191	10.2	63.7	37	1	US-07-718-274A-44	Sequence 56, Appl1
119	10.8	67.5	71	3	US-08-290-736C-47	Sequence 252, App	192	10.2	63.7	37	1	US-07-718-274A-44	Sequence 56, Appl1
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122	10.8	67.5	74	3	US-09-389-341-2	Sequence 6, Appl1	195	10.2	63.7	37	1	US-08-149-106-44	Sequence 56, Appl1
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124	10.6	66.2	76	4	US-09-548-260-6	Sequence 1, Appl1	197	10.2	63.7	37	1	US-08-298-021-56	Sequence 44, Appl1
125	10.6	66.2	87	3	US-09-390-867A-1	Sequence 1, Appl1	198	10.2	63.7	37	1	US-08-298-021-56	Sequence 56, Appl1
126	10.6	66.2	87	4	US-09-548-260-1	Sequence 68, Appl1	199	10.2	63.7	37	1	US-08-298-021-56	Sequence 62, Appl1
127	10.4	65.0	19	2	US-08-598-607-4	Sequence 15, Appl1	200	10.2	63.7	37	1	US-09-775-850-11	Sequence 5, Appl1
128	10.4	65.0	20	3	US-09-289-267-68	Sequence 88, Appl1	201	10.2	63.7	44	3	US-08-190-199A-5	Sequence 399, App
129	10.4	65.0	20	3	US-09-101-886B-88	Sequence 15, Appl1	202	10.2	63.7	46	2	US-08-190-199A-5	Sequence 59, Appl1
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131	10.4	65.0	21	3	US-08-109-037-88	Sequence 90, Appl1	204	10.2	63.7	86	1	US-07-964-624D-59	Sequence 59, Appl1
132	10.4	65.0	21	3	US-08-109-037-89	Sequence 90, Appl1	205	10.2	63.7	86	1	US-08-442-062-59	Sequence 59, Appl1
133	10.4	65.0	21	3	US-08-109-037-90	Sequence 3, Appl1	206	10.2	63.7	86	1	US-08-748-697A-59	Sequence 59, Appl1
134	10.4	65.0	23	1	US-08-244-269-3	Sequence 16, Appl1	207	10.2	63.7	86	4	US-09-165-616-59	Sequence 41, Appl1
135	10.4	65.0	23	1	US-08-348-683-16	Sequence 4, Appl1	208	10	62.5	17	3	US-09-027-998A-41	Sequence 57, Appl1
136	10.4	65.0	25	1	US-08-244-269-4	Sequence 18, Appl1	209	10	62.5	19	3	US-09-058-489-57	Sequence 52, Appl1
137	10.4	65.0	25	1	US-08-348-683-6	Sequence 18, Appl1	210	10	62.5	20	3	US-09-444-053-57	Sequence 51, Appl1
138	10.4	65.0	25	1	US-08-348-683-18	Sequence 19, Appl1	211	10	62.5	20	4	US-09-732-199A-51	Sequence 32, Appl1
139	10.4	65.0	25	1	US-08-348-683-19	Sequence 15, Appl1	212	10	62.5	21	3	US-09-253-025-32	Sequence 42, Appl1
140	10.4	65.0	30	1	US-08-049-473-15	Sequence 16, Appl1	213	10	62.5	21	3	US-09-027-998A-42	Sequence 26, Appl1
141	10.4	65.0	30	1	US-08-049-473-16	Sequence 15, Appl1	214	10	62.5	21	4	US-08-936-107A-26	Sequence 11, Appl1
142	10.4	65.0	30	1	US-08-312-648-15	Sequence 16, Appl1	215	10	62.5	23	2	US-08-880-829-11	Sequence 19, Appl1
143	10.4	65.0	30	1	US-08-312-648-16	Sequence 16, Appl1	216	10	62.5	24	2	US-08-880-829-17	Sequence 17, Appl1
144	10.4	65.0	30	3	US-09-176-862-7	Sequence 43, Appl1	217	10	62.5	24	2	US-08-880-829-11	Sequence 26, Appl1
145	10.4	65.0	30	3	US-09-202-316-43	Sequence 15, Appl1	218	10	62.5	25	3	US-08-986-727-26	Sequence 16, Appl1
146	10.4	65.0	30	5	PCT-US94-04190-15	Sequence 15, Appl1	219	10	62.5	26	4	US-09-534-638-16	Sequence 6, Appl1
147	10.4	65.0	30	5	PCT-US94-04190-16	Sequence 22, Appl1	220	10	62.5	26	4	US-09-732-199A-6	Sequence 7, Appl1
148	10.4	65.0	33	4	US-09-813-781-22	Sequence 13, Appl1	221	10	62.5	27	1	US-08-678-304-7	Sequence 8, Appl1
149	10.4	65.0	34	1	US-08-334-503-13	Sequence 15, Appl1	222	10	62.5	32	2	US-08-880-829-8	Sequence 12, Appl1
150	10.4	65.0	36	1	US-08-399-696-15	Sequence 4, Appl1	223	10	62.5	33	4	US-09-523-686-6	Sequence 11, Appl1
151	10.4	65.0	40	2	US-08-882-083-4	Sequence 4, Appl1	224	10	62.5	44	3	US-09-027-998A-12	Sequence 9, Appl1
152	10.4	65.0	40	2	US-08-558-107-4	Sequence 26, Appl1	225	10	62.5	44	3	US-09-027-998A-9	Sequence 10, Appl1
153	10.4	65.0	40	3	US-09-243-539-4	Sequence 56, Appl1	226	10	62.5	45	3	US-09-027-998A-10	Sequence 15, Appl1
154	10.4	65.0	46	1	US-07-994-469A-56	Sequence 959, App	227	10	62.5	45	3	US-09-027-998A-15	Sequence 55, Appl1
155	10.4	65.0	47	4	US-09-422-978-959	Sequence 1217, App	228	10	62.5	45	3	US-09-027-998A-16	Sequence 55, Appl1
156	10.4	65.0	47	4	US-09-422-978-1217	Sequence 124, App	229	10	62.5	50	1	US-08-530-492-55	Sequence 18, Appl1
157	10.4	65.0	48	2	US-08-811-492-124	Sequence 3, Appl1	230	10	62.5	50	3	US-09-027-998A-18	Sequence 19, Appl1
158	10.4	65.0	48	2	US-08-882-083-3	Sequence 3, Appl1	231	10	62.5	52	3	US-09-027-998A-19	Sequence 16, Appl1
159	10.4	65.0	48	2	US-08-558-107-3	Sequence 26, Appl1	232	10	62.5	52	3	US-09-027-998A-19	Sequence 16, Appl1
160	10.4	65.0	48	2	US-09-243-539-3	Sequence 26, Appl1	233	10	62.5	55	3	US-08-986-727-16	Sequence 14, Appl1
161	10.4	65.0	49	1	US-08-644-871-26	Sequence 27, Appl1	234	10	62.5	65	3	US-08-880-829-13	Sequence 12, Appl1
162	10.4	65.0	49	1	US-09-363-970-27	Sequence 23, Appl1	235	10	62.5	70	2	US-08-880-829-14	Sequence 12, Appl1
163	10.4	65.0	49	3	US-09-077-955-23	Sequence 25, Appl1	236	10	62.5	73	2	US-08-880-829-12	Sequence 10, Appl1
164	10.4	65.0	49	4	US-07-994-469A-25	Sequence 20, Appl1	237	10	62.5	79	1	US-07-982-712-10	Sequence 61, Appl1
165	10.4	65.0	50	1	US-08-445-640-20	Sequence 20, Appl1	238	10	62.5	80	3	US-08-311-446C-61	Sequence 2622, App
166	10.4	65.0	50	3	US-08-170-558-20	Sequence 20, Appl1	239	10	62.5	15	1	US-08-584-040-2622	Sequence 1146, App
167	10.4	65.0	50	3	US-08-447-314-20	Sequence 35, Appl1	240	10	62.5	17	4	US-09-371-772B-1147	Sequence 49, Appl1
168	10.4	65.0	50	3	US-08-445-641-20	Sequence 10, Appl1	241	9.8	61.3	17	4	US-09-371-772B-1147	Sequence 49, Appl1
169	10.4	65.0	52	1	US-07-994-469A-35	Sequence 11, Appl1	242	9.8	61.3	17	4	US-09-371-772B-1147	Sequence 49, Appl1
170	10.4	65.0	55	1	US-08-180-195-10	Sequence 10, Appl1	243	9.8	61.3	17	4	US-09-371-772B-1147	Sequence 49, Appl1
171	10.4	65.0	55	1	US-08-180-195-11	Sequence 10, Appl1	244	9.8	61.3	17	4	US-09-371-772B-1147	Sequence 49, Appl1
172	10.4	65.0	55	1	US-08-477-329-10	Sequence 10, Appl1	245	9.8	61.3	17	4	US-09-371-772B-1147	Sequence 49, Appl1
173	10.4	65.0	55	1	US-08-477-329-10	Sequence 10, Appl1	246	9.8	61.3	18	4	US-09-371-772B-1147	Sequence 49, Appl1

C 247	9.8	61.3	20	1	US-07-977-284A-39	Sequence 39, Appl	320	9.8	61.3	51	4	US-09-393-385B-7	Sequence 7, Appl
C 248	9.8	61.3	20	2	US-08-468-551-1	Sequence 1, Appl	321	9.8	61.3	51	4	US-09-394-455-55	Sequence 55, Appl
C 249	9.8	61.3	20	2	US-08-256-426B-39	Sequence 39, Appl	C 322	9.8	61.3	54	1	US-08-353-400-11	Sequence 11, Appl
C 250	9.8	61.3	20	3	US-09-280-799-83	Sequence 83, Appl	C 323	9.8	61.3	54	1	US-08-353-400-12	Sequence 12, Appl
C 251	9.8	61.3	20	3	US-09-560-594-49	Sequence 49, Appl	C 324	9.8	61.3	54	4	US-09-479-645A-169	Sequence 169, Appl
C 252	9.8	61.3	20	3	US-09-657-346A-33	Sequence 33, Appl	C 325	9.8	61.3	54	4	US-09-479-645A-175	Sequence 175, Appl
C 253	9.8	61.3	20	4	US-09-422-978-3992	Sequence 3992, Ap	C 326	9.8	61.3	59	1	US-08-160-670A-35	Sequence 35, Appl
C 254	9.8	61.3	20	4	US-09-920-759-87	Sequence 87, Appl	C 327	9.8	61.3	71	4	US-09-301-593-87	Sequence 87, Appl
C 255	9.8	61.3	20	4	US-09-060-299-378	Sequence 378, App	C 328	9.8	61.3	72	1	US-08-105-483-211	Sequence 211, App
C 256	9.8	61.3	20	4	US-09-402-923A-378	Sequence 378, App	C 329	9.8	61.3	72	1	US-08-105-483-212	Sequence 212, App
C 257	9.8	61.3	21	1	US-08-435-480-6	Sequence 6, Appl	C 330	9.8	61.3	72	1	US-08-303-124-10	Sequence 10, Appl
C 258	9.8	61.3	21	2	US-08-946-241B-6	Sequence 6, Appl	C 331	9.8	61.3	72	1	US-08-303-124-11	Sequence 11, Appl
C 259	9.8	61.3	21	3	US-09-309-053-6	Sequence 6, Appl	C 332	9.8	61.3	72	1	US-08-204-729-10	Sequence 10, Appl
C 260	9.8	61.3	21	3	US-08-557-614-8	Sequence 8, Appl	C 333	9.8	61.3	72	1	US-08-204-729-11	Sequence 11, Appl
C 261	9.8	61.3	21	3	US-09-394-455-41	Sequence 41, Appl	C 334	9.8	61.3	72	1	US-08-475-063-28	Sequence 28, Appl
C 262	9.8	61.3	22	3	US-09-103-875-101	Sequence 101, App	C 335	9.8	61.3	72	1	US-08-207-792-28	Sequence 28, Appl
C 263	9.8	61.3	23	2	US-08-839-306-5	Sequence 5, Appl	C 336	9.8	61.3	72	1	US-08-709-209-211	Sequence 211, App
C 264	9.8	61.3	23	3	US-08-978-454-5	Sequence 5, Appl	C 337	9.8	61.3	72	1	US-08-709-209-212	Sequence 212, App
C 265	9.8	61.3	23	3	US-09-385-288-5	Sequence 5, Appl	C 338	9.8	61.3	72	1	US-08-458-101-211	Sequence 211, App
C 266	9.8	61.3	24	3	US-09-670-075A-11	Sequence 11, Appl	C 339	9.8	61.3	72	1	US-08-458-101-212	Sequence 212, App
C 267	9.8	61.3	25	1	US-08-336-132-8	Sequence 8, Appl	C 340	9.8	61.3	72	2	US-08-480-697B-10	Sequence 10, Appl
C 268	9.8	61.3	25	3	US-09-012-097A-15	Sequence 15, Appl	C 341	9.8	61.3	72	2	US-08-480-697B-11	Sequence 11, Appl
C 269	9.8	61.3	25	3	US-08-672-213-36	Sequence 36, Appl	C 342	9.8	61.3	73	1	US-08-475-063-29	Sequence 29, Appl
C 270	9.8	61.3	25	4	US-09-538-709-301	Sequence 301, App	C 343	9.8	61.3	73	1	US-08-207-792-29	Sequence 29, Appl
C 271	9.8	61.3	25	4	US-09-481-620A-31	Sequence 31, Appl	C 344	9.8	61.3	75	1	US-08-219-012-85	Sequence 85, Appl
C 272	9.8	61.3	27	2	US-08-232-081B-32	Sequence 32, Appl	C 345	9.8	61.3	75	1	US-08-219-012-85	Sequence 85, Appl
C 273	9.8	61.3	28	1	US-08-221-078A-1	Sequence 1, Appl	C 346	9.8	61.3	75	3	US-08-687-421-273	Sequence 273, App
C 274	9.8	61.3	28	1	US-08-221-171A-1	Sequence 1, Appl	C 347	9.8	61.3	75	3	US-08-687-421-276	Sequence 276, App
C 275	9.8	61.3	29	1	US-08-217-210B-26	Sequence 26, Appl	C 348	9.8	61.3	76	1	US-08-657-012-6	Sequence 6, Appl
C 276	9.8	61.3	29	4	US-08-054-970-4	Sequence 4, Appl	C 349	9.8	61.3	76	3	US-09-013-872-6	Sequence 6, Appl
C 277	9.8	61.3	29	4	US-09-304-232-853	Sequence 853, App	C 350	9.8	61.3	76	3	US-09-184-192-85	Sequence 85, Appl
C 278	9.8	61.3	30	1	US-08-160-670A-39	Sequence 39, Appl	C 351	9.8	61.3	76	4	US-09-633-653-6	Sequence 6, Appl
C 279	9.8	61.3	30	1	US-08-384-708A-9	Sequence 9, Appl	C 352	9.8	61.3	77	1	US-08-633-653-6	Sequence 6, Appl
C 280	9.8	61.3	30	1	US-08-322-677A-13	Sequence 13, Appl	C 353	9.8	61.3	77	1	US-08-384-708A-190	Sequence 190, App
C 281	9.8	61.3	30	1	US-08-322-676-13	Sequence 13, Appl	C 354	9.8	61.3	77	3	US-08-687-421-282	Sequence 282, App
C 282	9.8	61.3	30	2	US-08-600-999-3	Sequence 3, Appl	C 355	9.8	61.3	78	4	US-08-653-648A-47	Sequence 47, Appl
C 283	9.8	61.3	30	3	US-08-898-218-13	Sequence 13, Appl	C 356	9.8	61.3	81	2	US-08-116-778E-26	Sequence 26, Appl
C 284	9.8	61.3	30	3	US-08-848-793-13	Sequence 13, Appl	C 357	9.8	61.3	81	2	US-08-438-562-26	Sequence 26, Appl
C 285	9.8	61.3	30	3	US-08-687-421-9	Sequence 9, Appl	C 358	9.8	61.3	81	2	US-08-483-528B-26	Sequence 26, Appl
C 286	9.8	61.3	30	4	US-09-937-832-2	Sequence 2, Appl	C 359	9.8	61.3	81	3	US-08-673-799C-26	Sequence 26, Appl
C 287	9.8	61.3	30	4	US-08-322-678-13	Sequence 13, Appl	C 360	9.8	61.3	81	4	US-09-393-385B-26	Sequence 26, Appl
C 288	9.8	61.3	31	2	US-08-600-999-11	Sequence 11, Appl	C 361	9.8	61.3	82	3	US-08-468-551B-647	Sequence 647, App
C 289	9.8	61.3	31	3	US-08-732-218-10	Sequence 10, Appl	C 362	9.8	61.3	86	5	PCT-US96-00952-13	Sequence 13, Appl
C 290	9.8	61.3	31	3	US-08-523-894-57	Sequence 57, Appl	C 363	9.8	61.3	86	5	PCT-US94-07779-19	Sequence 19, Appl
C 291	9.8	61.3	32	4	US-09-420-819-8	Sequence 8, Appl	C 364	9.8	61.3	87	5	PCT-US95-05600-6	Sequence 6, Appl
C 292	9.8	61.3	35	1	US-08-328-592-9	Sequence 9, Appl	C 365	9.8	61.3	87	5	PCT-US95-05600-11	Sequence 11, Appl
C 293	9.8	61.3	35	3	US-09-439-000-3	Sequence 3, Appl	C 366	9.8	61.3	87	5	PCT-US96-00952-14	Sequence 14, Appl
C 294	9.8	61.3	36	3	US-08-746-883-9	Sequence 9, Appl	C 367	9.8	61.3	93	3	US-08-943-731-16	Sequence 16, Appl
C 295	9.8	61.3	37	3	US-09-366-009-18	Sequence 18, Appl	C 368	9.8	61.3	94	2	US-08-483-528B-57	Sequence 57, Appl
C 296	9.8	61.3	37	4	US-08-809-156B-18	Sequence 18, Appl	C 369	9.8	61.3	94	3	US-08-673-799C-57	Sequence 57, Appl
C 297	9.8	61.3	39	1	US-08-253-155A-83	Sequence 83, Appl	C 370	9.8	61.3	94	3	US-09-393-385B-57	Sequence 57, Appl
C 298	9.8	61.3	39	1	US-08-625-209A-12	Sequence 12, Appl	C 371	9.8	61.3	94	4	US-08-162-961B-6	Sequence 6, Appl
C 299	9.8	61.3	39	3	US-08-853-733B-12	Sequence 12, Appl	C 372	9.8	61.3	99	4	US-09-007-678B-9	Sequence 9, Appl
C 300	9.8	61.3	39	3	US-07-987-264-37	Sequence 37, Appl	C 373	9.8	61.3	100	4	US-08-706-945D-91	Sequence 91, Appl
C 301	9.8	61.3	39	3	US-07-987-264-37	Sequence 37, Appl	C 374	9.6	60.0	10	3	US-09-581-326-13	Sequence 13, Appl
C 302	9.8	61.3	40	4	US-09-538-709-1193	Sequence 1193, Ap	C 375	9.6	60.0	10	3	US-09-581-326-18	Sequence 18, Appl
C 303	9.8	61.3	41	3	US-08-813-507-115	Sequence 115, App	C 376	9.6	60.0	10	4	US-09-907-074A-13	Sequence 13, Appl
C 304	9.8	61.3	41	4	US-09-464-453-135	Sequence 135, App	C 377	9.6	60.0	10	4	US-09-907-074A-18	Sequence 18, Appl
C 305	9.8	61.3	42	1	US-08-271-880A-52	Sequence 52, Appl	C 378	9.6	60.0	29	4	US-09-304-232A-104	Sequence 204, App
C 306	9.8	61.3	42	2	US-08-910-408-52	Sequence 52, Appl	C 379	9.6	60.0	30	3	US-09-136-605-15	Sequence 15, Appl
C 307	9.8	61.3	42	2	US-09-249-215-52	Sequence 52, Appl	C 380	9.6	60.0	36	3	US-09-026-958-11	Sequence 11, Appl
C 308	9.8	61.3	44	6	5252466-21	Patent No. 5252466	C 381	9.6	60.0	36	4	US-09-390-207-19	Sequence 19, Appl
C 309	9.8	61.3	47	4	US-09-422-978-2991	Sequence 2991, Ap	C 382	9.6	60.0	46	3	US-08-997-918-17	Sequence 17, Appl
C 310	9.8	61.3	47	4	US-09-422-978-3652	Sequence 3652, Ap	C 383	9.6	60.0	47	4	US-09-422-978-1615	Sequence 1615, App
C 311	9.8	61.3	48	4	US-09-063-893A-18	Sequence 18, Appl	C 384	9.6	60.0	50	1	US-08-753-054-6	Sequence 6, Appl
C 312	9.8	61.3	49	4	US-09-061-154-8	Sequence 8, Appl	C 385	9.6	60.0	53	1	US-07-778-233B-68	Sequence 68, Appl
C 313	9.8	61.3	50	4	US-09-538-709-957	Sequence 957, App	C 386	9.6	60.0	53	1	US-07-963-321-68	Sequence 68, Appl
C 314	9.8	61.3	50	4	US-08-832-468-6	Sequence 46, Appl	C 387	9.6	60.0	53	1	US-08-290-641-68	Sequence 68, Appl
C 315	9.8	61.3	51	2	US-08-116-778E-42	Sequence 42, Appl	C 388	9.6	60.0	53	1	US-08-548-540-68	Sequence 68, Appl
C 316	9.8	61.3	51	2	US-08-438-562-42	Sequence 42, Appl	C 389	9.6	60.0	53	5	PCT-US96-09809-68	Sequence 68, Appl
C 317	9.8	61.3	51	2	US-08-483-528B-7	Sequence 7, Appl	C 390	9.6	60.0	80	1	US-08-468-275-1	Sequence 1, Appl
C 318	9.8	61.3	51	3	US-08-673-799C-7	Sequence 7, Appl	C 391	9.6	60.0	80	4	US-09-007-466-1	Sequence 1, Appl
C 319	9.8	61.3	51	3	US-07-987-264-8	Sequence 8, Appl	C 392	9.6	60.0	80	4	US-08-952-980B-1	Sequence 1, Appl

393	9.6	60.0	91	1	US-08-142-551B-129	Sequence 129, App	466	9.4	58.8	27	4	US-09-538-709-179	Sequence 179, App
394	9.6	60.0	91	1	US-08-142-551B-130	Sequence 130, App	467	9.4	58.8	27	5	PCT-US93-08435-38	Sequence 38, App
395	9.6	60.0	96	3	US-08-484-322-35	Sequence 35, App	468	9.4	58.8	28	1	US-07-959-369-18	Sequence 18, App
396	9.4	58.8	17	1	US-08-373-124A-4441	Sequence 1441, Ap	469	9.4	58.8	29	1	US-07-805-567-24	Sequence 24, App
397	9.4	58.8	17	1	US-08-435-628-1441	Sequence 1441, Ap	470	9.4	58.8	29	1	US-08-105-483-106	Sequence 106, App
398	9.4	58.8	17	4	US-08-584-040-2621	Sequence 2621, Ap	471	9.4	58.8	29	1	US-08-220-151-63	Sequence 63, App
399	9.4	58.8	17	4	US-09-371-772B-1145	Sequence 1145, Ap	472	9.4	58.8	29	1	US-08-413-118-63	Sequence 63, App
400	9.4	58.8	17	4	US-09-371-772B-5482	Sequence 5482, Ap	473	9.4	58.8	29	1	US-08-224-657-40	Sequence 40, App
401	9.4	58.8	17	6	5176995-4	Patent No. 5176995	474	9.4	58.8	29	1	US-08-709-209-106	Sequence 106, App
402	9.4	58.8	18	1	US-08-468-580-28	Sequence 28, App	475	9.4	58.8	29	1	US-08-458-101-106	Sequence 106, App
403	9.4	58.8	18	3	US-08-643-212-50	Sequence 50, App	476	9.4	58.8	29	2	US-08-184-009-39	Sequence 39, App
404	9.4	58.8	18	4	US-09-242-937-3	Sequence 3, App	477	9.4	58.8	29	2	US-08-486-969-28	Sequence 28, App
405	9.4	58.8	18	4	US-09-422-978-10236	Sequence 10236, A	478	9.4	58.8	29	2	US-08-417-210A-39	Sequence 39, App
406	9.4	58.8	18	5	PCT-US95-03731-28	Sequence 28, App	479	9.4	58.8	29	2	US-08-458-356-33	Sequence 33, App
407	9.4	58.8	19	1	US-08-379-081B-141	Sequence 141, App	480	9.4	58.8	29	2	US-08-471-025-28	Sequence 28, App
408	9.4	58.8	19	1	US-08-379-081B-142	Sequence 142, App	481	9.4	58.8	29	2	US-08-471-025-28	Sequence 28, App
409	9.4	58.8	19	1	US-08-379-081B-143	Sequence 143, App	482	9.4	58.8	29	3	US-08-473-446-63	Sequence 63, App
410	9.4	58.8	19	1	US-08-379-078-141	Sequence 141, App	483	9.4	58.8	29	3	US-08-460-736-39	Sequence 39, App
411	9.4	58.8	19	1	US-08-379-078-142	Sequence 142, App	484	9.4	58.8	29	3	US-09-085-273-28	Sequence 28, App
412	9.4	58.8	19	1	US-08-379-078-143	Sequence 143, App	485	9.4	58.8	29	4	US-09-354-138-40	Sequence 40, App
413	9.4	58.8	19	3	US-08-749-157-8	Sequence 8, App	486	9.4	58.8	29	4	US-09-535-370-39	Sequence 39, App
414	9.4	58.8	19	4	US-09-302-681-79	Sequence 79, App	487	9.4	58.8	29	5	PCT-US96-00547-28	Sequence 28, App
415	9.4	58.8	20	2	US-08-484-985-43	Sequence 43, App	488	9.4	58.8	30	1	US-08-182-530-4	Sequence 4, App
416	9.4	58.8	20	2	US-08-757-653-43	Sequence 52, App	489	9.4	58.8	30	1	US-08-050-058B-4	Sequence 4, App
417	9.4	58.8	20	3	US-09-428-696-52	Sequence 183, App	490	9.4	58.8	30	1	US-08-737-757-5	Sequence 5, App
418	9.4	58.8	20	3	US-09-311-260-183	Sequence 120, App	491	9.4	58.8	30	1	US-08-463-587A-4	Sequence 4, App
419	9.4	58.8	20	4	US-09-171-945-120	Sequence 43, App	492	9.4	58.8	30	2	US-08-463-667A-7	Sequence 7, App
420	9.4	58.8	20	4	US-08-520-946-43	Sequence 23, App	493	9.4	58.8	30	2	US-08-683-743-14	Sequence 14, App
421	9.4	58.8	20	4	US-09-732-199A-23	Sequence 76, App	494	9.4	58.8	30	2	US-08-441-871-8	Sequence 8, App
422	9.4	58.8	20	4	US-09-011-769A-76	Sequence 2909, Ap	495	9.4	58.8	30	3	US-08-923-854-4	Sequence 4, App
423	9.4	58.8	20	4	US-09-198-452A-2309	Sequence 3607, Ap	496	9.4	58.8	30	3	US-09-171-945-121	Sequence 121, App
424	9.4	58.8	20	4	US-09-198-452A-3607	Sequence 5879, Ap	497	9.4	58.8	30	4	US-09-011-769A-77	Sequence 78, App
425	9.4	58.8	20	4	US-09-198-452A-5879	Sequence 6215, Ap	498	9.4	58.8	30	5	PCT-US91-09133-4	Sequence 4, App
426	9.4	58.8	20	4	US-09-198-452A-6756	Sequence 6756, Ap	499	9.4	58.8	31	3	US-08-281-313-3	Sequence 3, App
427	9.4	58.8	20	4	US-09-460-555-6	Sequence 6, App	500	9.4	58.8	31	3	US-09-007-288E-106	Sequence 106, App
428	9.4	58.8	21	1	US-08-598-591-46	Sequence 46, App	501	9.4	58.8	32	4	US-09-443-800-4	Sequence 4, App
429	9.4	58.8	21	1	US-08-798-691-50	Sequence 50, App	502	9.4	58.8	33	4	US-09-587-835B-4	Sequence 4, App
430	9.4	58.8	21	1	US-08-782-047-12	Sequence 12, App	503	9.4	58.8	33	4	US-08-110-161A-14	Sequence 14, App
431	9.4	58.8	21	1	US-08-749-431A-12	Sequence 7, App	504	9.4	58.8	34	5	PCT-US94-09350-14	Sequence 14, App
432	9.4	58.8	21	2	US-08-600-999-7	Sequence 9, App	505	9.4	58.8	34	5	US-08-147-000B-14	Sequence 14, App
433	9.4	58.8	21	2	US-08-825-487A-50	Sequence 50, App	506	9.4	58.8	36	2	US-08-792-055-4	Sequence 4, App
434	9.4	58.8	21	2	US-08-825-487A-86	Sequence 86, App	507	9.4	58.8	36	2	US-08-330-888A-3	Sequence 3, App
435	9.4	58.8	21	3	US-09-074-476-50	Sequence 56, App	508	9.4	58.8	36	2	US-08-657-641-8	Sequence 8, App
436	9.4	58.8	21	3	US-08-924-870A-12	Sequence 12, App	509	9.4	58.8	36	2	US-09-892-074-10	Sequence 10, App
437	9.4	58.8	21	3	US-08-111-077-62	Sequence 62, App	510	9.4	58.8	36	5	PCT-US94-07233-8	Sequence 8, App
438	9.4	58.8	22	1	US-08-951-718-15	Sequence 15, App	511	9.4	58.8	38	3	US-08-930-589A-16	Sequence 16, App
439	9.4	58.8	22	2	5219727-31	Patent No. 5219727	512	9.4	58.8	39	1	US-08-458-067-17	Sequence 17, App
440	9.4	58.8	22	2	US-09-011-600-2	Sequence 2, App	513	9.4	58.8	39	1	US-08-231-342-18	Sequence 18, App
441	9.4	58.8	22	6	US-09-722-348-2	Sequence 2, App	514	9.4	58.8	40	1	US-08-428-137-3	Sequence 3, App
442	9.4	58.8	24	3	US-09-600-031-9	Sequence 9, App	515	9.4	58.8	40	5	US-08-485-180-3	Sequence 3, App
443	9.4	58.8	24	4	US-09-538-709-229	Sequence 229, App	516	9.4	58.8	40	5	US-08-419-765-3	Sequence 3, App
444	9.4	58.8	24	4	US-09-216-393B-355	Sequence 359, App	517	9.4	58.8	41	4	US-08-753-054-9	Sequence 9, App
445	9.4	58.8	24	4	US-08-382-933-3	Sequence 3, App	518	9.4	58.8	41	4	US-08-741-881-108	Sequence 108, App
446	9.4	58.8	25	1	US-08-147-000B-7	Sequence 7, App	519	9.4	58.8	45	1	US-08-739-158-108	Sequence 108, App
447	9.4	58.8	25	1	US-08-479-596A-13	Sequence 13, App	520	9.4	58.8	45	1	US-08-739-158-108	Sequence 108, App
448	9.4	58.8	25	2	US-08-726-090-7	Sequence 28, App	521	9.4	58.8	45	1	US-08-404-796-108	Sequence 108, App
449	9.4	58.8	25	2	US-08-094-128A-28	Sequence 28, App	522	9.4	58.8	45	1	US-09-350-359-108	Sequence 108, App
450	9.4	58.8	26	1	US-08-455-674-28	Sequence 34, App	523	9.4	58.8	45	1	US-07-805-567-22	Sequence 22, App
451	9.4	58.8	26	1	US-08-450-257-34	Sequence 34, App	524	9.4	58.8	46	1	US-08-105-483-107	Sequence 107, App
452	9.4	58.8	26	1	US-08-450-257-34	Sequence 34, App	525	9.4	58.8	46	1	US-08-073-962-15	Sequence 15, App
453	9.4	58.8	26	1	US-08-455-992-28	Sequence 28, App	526	9.4	58.8	46	1	US-08-220-151-64	Sequence 64, App
454	9.4	58.8	26	1	US-08-455-992-28	Sequence 28, App	527	9.4	58.8	46	1	US-08-413-118-60	Sequence 60, App
455	9.4	58.8	26	1	US-08-455-992-28	Sequence 28, App	528	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
456	9.4	58.8	26	1	US-08-455-992-28	Sequence 28, App	529	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
457	9.4	58.8	26	1	US-08-450-246-34	Sequence 34, App	530	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
458	9.4	58.8	26	1	US-08-450-246-34	Sequence 34, App	531	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
459	9.4	58.8	26	1	US-08-450-246-34	Sequence 34, App	532	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
460	9.4	58.8	26	1	US-08-450-246-34	Sequence 34, App	533	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
461	9.4	58.8	26	1	US-08-690-734A-21	Sequence 21, App	534	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
462	9.4	58.8	26	2	US-08-742-185-21	Sequence 21, App	535	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
463	9.4	58.8	26	3	US-08-235-403-34	Sequence 34, App	536	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
464	9.4	58.8	26	5	PCT-US92-00652-28	Sequence 28, App	537	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App
465	9.4	58.8	27	2	US-08-545-562A-62	Sequence 62, App	538	9.4	58.8	46	1	US-08-224-657-40	Sequence 40, App

C 539	9.4	58.8	46	1	US-08-484-304-60	Sequence 60, Appl	C 612	9.4	58.8	70	1	US-08-105-483-457	Sequence 457, App
C 540	9.4	58.8	46	1	US-08-224-657-41	Sequence 41, Appl	C 613	9.4	58.8	70	1	US-08-303-124-13	Sequence 13, Appl
C 541	9.4	58.8	46	1	US-08-487-412-15	Sequence 15, Appl	C 614	9.4	58.8	70	1	US-08-475-063-42	Sequence 42, Appl
C 542	9.4	58.8	46	1	US-08-709-209-107	Sequence 107, App	C 615	9.4	58.8	70	1	US-08-207-792-42	Sequence 42, Appl
C 543	9.4	58.8	46	1	US-08-458-101-107	Sequence 101, App	C 616	9.4	58.8	70	1	US-08-709-209-457	Sequence 457, App
C 544	9.4	58.8	46	2	US-08-184-009-40	Sequence 40, Appl	C 617	9.4	58.8	70	1	US-08-303-165-169	Sequence 165, App
C 545	9.4	58.8	46	2	US-08-486-969-29	Sequence 29, Appl	C 618	9.4	58.8	70	1	US-08-458-101-457	Sequence 457, App
C 546	9.4	58.8	46	2	US-08-417-210A-40	Sequence 40, Appl	C 619	9.4	58.8	70	2	US-08-480-697B-13	Sequence 13, Appl
C 547	9.4	58.8	46	2	US-08-458-356-40	Sequence 40, Appl	C 620	9.4	58.8	71	1	US-08-081-539-43	Sequence 43, Appl
C 548	9.4	58.8	46	2	US-08-471-025-29	Sequence 29, Appl	C 621	9.4	58.8	71	1	US-08-466-647-43	Sequence 43, Appl
C 549	9.4	58.8	46	2	US-08-658-665-29	Sequence 29, Appl	C 622	9.4	58.8	72	1	US-08-105-483-211	Sequence 211, App
C 550	9.4	58.8	46	3	US-08-473-446-64	Sequence 64, Appl	C 623	9.4	58.8	72	1	US-08-105-483-212	Sequence 212, App
C 551	9.4	58.8	46	3	US-08-460-736-40	Sequence 40, Appl	C 624	9.4	58.8	72	1	US-08-303-124-10	Sequence 10, Appl
C 552	9.4	58.8	46	3	US-09-085-273-29	Sequence 29, Appl	C 625	9.4	58.8	72	1	US-08-303-124-11	Sequence 11, Appl
C 553	9.4	58.8	46	4	US-09-354-138-41	Sequence 41, Appl	C 626	9.4	58.8	72	1	US-08-204-129-10	Sequence 10, Appl
C 554	9.4	58.8	46	4	US-09-535-370-40	Sequence 40, Appl	C 627	9.4	58.8	72	1	US-08-204-129-11	Sequence 11, Appl
C 555	9.4	58.8	46	5	PCT-US96-00547-29	Sequence 29, Appl	C 628	9.4	58.8	72	1	US-08-475-063-38	Sequence 28, Appl
C 556	9.4	58.8	47	4	US-09-422-978-1577	Sequence 1577, Ap	C 629	9.4	58.8	72	1	US-08-207-792-28	Sequence 28, Appl
C 557	9.4	58.8	47	4	US-09-422-978-1553	Sequence 1553, Ap	C 630	9.4	58.8	72	1	US-08-709-209-211	Sequence 211, App
C 558	9.4	58.8	47	4	US-09-422-978-1834	Sequence 1834, Ap	C 631	9.4	58.8	72	1	US-08-709-209-212	Sequence 212, App
C 559	9.4	58.8	47	4	US-09-422-978-2810	Sequence 2810, Ap	C 632	9.4	58.8	72	1	US-08-458-101-211	Sequence 211, App
C 560	9.4	58.8	48	1	US-07-842-089B-6	Sequence 6, Appli	C 633	9.4	58.8	72	1	US-08-458-101-212	Sequence 212, App
C 561	9.4	58.8	48	1	US-08-264-485-6	Sequence 6, Appli	C 634	9.4	58.8	72	2	US-08-480-697B-10	Sequence 10, Appl
C 562	9.4	58.8	48	2	US-08-629-039-9	Sequence 9, Appli	C 635	9.4	58.8	72	2	US-08-480-697B-11	Sequence 11, Appl
C 563	9.4	58.8	48	2	US-08-629-039-9	Sequence 9, Appli	C 636	9.4	58.8	72	3	US-09-367-953B-8	Sequence 8, Appli
C 564	9.4	58.8	48	2	US-08-629-039-10	Sequence 10, Appl	C 637	9.4	58.8	73	1	US-08-475-063-39	Sequence 29, Appl
C 565	9.4	58.8	48	5	PCT-US96-07795-16	Sequence 16, Appl	C 638	9.4	58.8	73	1	US-08-207-792-29	Sequence 29, Appl
C 566	9.4	58.8	48	5	PCT-US96-07796-16	Sequence 16, Appl	C 639	9.4	58.8	75	1	US-07-973-333-18	Sequence 18, Appl
C 567	9.4	58.8	50	1	US-07-805-567-23	Sequence 23, Appl	C 640	9.4	58.8	75	1	US-08-081-539-42	Sequence 42, Appl
C 568	9.4	58.8	50	1	US-08-105-483-108	Sequence 108, App	C 641	9.4	58.8	75	1	US-08-466-647-42	Sequence 42, Appl
C 569	9.4	58.8	50	1	US-08-073-962-16	Sequence 16, Appl	C 642	9.4	58.8	75	1	US-08-219-012-18	Sequence 18, Appl
C 570	9.4	58.8	50	1	US-08-220-151-65	Sequence 65, Appl	C 643	9.4	58.8	75	3	US-08-687-421-206	Sequence 206, App
C 571	9.4	58.8	50	1	US-08-413-118-65	Sequence 65, Appl	C 644	9.4	58.8	75	3	US-09-476-239-14	Sequence 14, Appl
C 572	9.4	58.8	50	1	US-08-224-331-61	Sequence 61, Appl	C 645	9.4	58.8	75	4	US-09-609-154-14	Sequence 14, Appl
C 573	9.4	58.8	50	1	US-08-484-304-61	Sequence 61, Appl	C 646	9.4	58.8	76	1	US-08-430-709-3	Sequence 3, Appli
C 574	9.4	58.8	50	1	US-08-224-657-42	Sequence 42, Appl	C 647	9.4	58.8	76	2	US-09-918-304A-3	Sequence 3, Appli
C 575	9.4	58.8	50	1	US-08-487-412-16	Sequence 16, Appl	C 648	9.4	58.8	76	3	US-09-407-234-1	Sequence 1, Appli
C 576	9.4	58.8	50	1	US-08-709-209-108	Sequence 108, App	C 649	9.4	58.8	78	2	US-08-430-709-15	Sequence 15, Appl
C 577	9.4	58.8	50	1	US-08-458-101-108	Sequence 108, App	C 650	9.4	58.8	78	2	US-08-918-304A-15	Sequence 15, Appl
C 578	9.4	58.8	50	2	US-08-184-009-41	Sequence 41, Appl	C 651	9.4	58.8	78	3	US-09-407-234-15	Sequence 15, Appl
C 579	9.4	58.8	50	2	US-08-486-969-30	Sequence 30, Appl	C 652	9.4	58.8	78	4	US-08-653-648A-48	Sequence 48, Appl
C 580	9.4	58.8	50	2	US-08-417-210A-41	Sequence 41, Appl	C 653	9.4	58.8	79	1	US-08-384-708A-210	Sequence 210, App
C 581	9.4	58.8	50	2	US-08-458-356-41	Sequence 41, Appl	C 654	9.4	58.8	79	2	US-08-470-939-8	Sequence 8, Appli
C 582	9.4	58.8	50	2	US-08-471-025-30	Sequence 30, Appl	C 655	9.4	58.8	79	3	US-08-687-421-102	Sequence 302, App
C 583	9.4	58.8	50	2	US-08-658-665-30	Sequence 30, Appl	C 656	9.4	58.8	79	5	PCT-US96-09452-8	Sequence 8, Appli
C 584	9.4	58.8	50	3	US-08-473-446-65	Sequence 65, Appl	C 657	9.4	58.8	80	1	US-08-472-255A-149	Sequence 149, App
C 585	9.4	58.8	50	3	US-09-012-097A-18	Sequence 18, Appl	C 658	9.4	58.8	80	1	US-08-479-724A-149	Sequence 149, App
C 586	9.4	58.8	50	3	US-08-460-736-41	Sequence 41, Appl	C 659	9.4	58.8	80	3	US-08-472-256B-149	Sequence 149, App
C 587	9.4	58.8	50	3	US-09-085-273-10	Sequence 30, Appl	C 660	9.4	58.8	80	3	US-08-952-793-149	Sequence 149, App
C 588	9.4	58.8	50	3	US-09-390-867A-40	Sequence 40, Appl	C 661	9.4	58.8	80	4	US-09-849-928-149	Sequence 149, App
C 589	9.4	58.8	50	4	US-09-354-138-42	Sequence 42, Appl	C 662	9.4	58.8	80	5	PCT-US96-09455A-149	Sequence 149, App
C 590	9.4	58.8	50	4	US-09-548-260-40	Sequence 40, Appl	C 663	9.4	58.8	81	1	US-08-472-255A-151	Sequence 151, App
C 591	9.4	58.8	50	4	US-09-535-370-41	Sequence 41, Appl	C 664	9.4	58.8	81	1	US-08-479-724A-151	Sequence 151, App
C 592	9.4	58.8	50	5	PCT-US96-00547-30	Sequence 30, Appl	C 665	9.4	58.8	81	3	US-08-472-256B-151	Sequence 151, App
C 593	9.4	58.8	51	3	US-09-367-953B-3	Sequence 3, Appli	C 666	9.4	58.8	81	3	US-08-952-793-151	Sequence 151, App
C 594	9.4	58.8	53	4	US-09-132-316-6	Sequence 6, Appli	C 667	9.4	58.8	81	4	US-09-849-928-151	Sequence 151, App
C 595	9.4	58.8	54	4	US-08-679-645-640	Sequence 640, App	C 668	9.4	58.8	81	5	PCT-US96-09455A-151	Sequence 151, App
C 596	9.4	58.8	57	1	US-07-916-034-18	Sequence 18, Appl	C 669	9.4	58.8	87	1	US-07-842-089B-26	Sequence 26, Appl
C 597	9.4	58.8	60	3	US-08-814-052-35	Sequence 35, Appl	C 670	9.4	58.8	87	1	US-08-264-485-16	Sequence 16, Appl
C 598	9.4	58.8	60	3	US-08-812-829-27	Sequence 27, Appl	C 671	9.4	58.8	89	3	US-09-367-953B-5	Sequence 5, Appli
C 599	9.4	58.8	61	3	US-08-986-727-18	Sequence 18, Appl	C 672	9.4	58.8	91	1	US-07-842-089B-25	Sequence 25, Appl
C 600	9.4	58.8	61	4	US-09-619-213B-83	Sequence 83, Appl	C 673	9.4	58.8	91	1	US-08-264-485-25	Sequence 25, Appl
C 601	9.4	58.8	63	2	US-08-472-171-6	Sequence 6, Appli	C 674	9.4	58.8	94	4	US-09-557-030G-258	Sequence 258, App
C 602	9.4	58.8	63	2	US-08-894-526-6	Sequence 6, Appli	C 675	9.4	57.5	15	1	US-08-182-368A-386	Sequence 386, App
C 603	9.4	58.8	63	2	US-09-013-047-6	Sequence 6, Appli	C 676	9.2	57.5	15	1	US-08-311-886C-580	Sequence 580, App
C 604	9.4	58.8	63	3	US-09-374-597-6	Sequence 6, Appli	C 677	9.2	57.5	15	2	US-08-774-306A-386	Sequence 386, App
C 605	9.4	58.8	68	2	US-08-459-135A-3	Sequence 3, Appli	C 678	9.2	57.5	15	4	US-09-064-156A-386	Sequence 386, App
C 606	9.4	58.8	68	2	US-08-495-559-3	Sequence 3, Appli	C 679	9.2	57.5	18	4	US-09-486-694B-102	Sequence 102, App
C 607	9.4	58.8	68	3	US-09-367-953B-10	Sequence 10, Appl	C 680	9.2	57.5	19	1	US-08-460-853-11	Sequence 11, Appl
C 608	9.4	58.8	69	2	US-08-472-171-13	Sequence 13, Appl	C 681	9.2	57.5	19	2	US-08-639-501-106	Sequence 106, App
C 609	9.4	58.8	69	2	US-08-894-526-13	Sequence 13, Appl	C 682	9.2	57.5	19	3	US-09-044-946-106	Sequence 106, App
C 610	9.4	58.8	69	2	US-09-013-047-13	Sequence 13, Appl	C 683	9.2	57.5	19	3	US-09-044-908-106	Sequence 106, App
C 611	9.4	58.8	69	3	US-09-374-597-13	Sequence 13, Appl	C 684	9.2	57.5	19	4	US-09-358-036-11	Sequence 11, Appl

C 685	9.2	57.5	19	4	US-09-298-745-23	Sequence 23, Appl	C 758	9.2	57.5	26	4	US-09-538-709-34	Sequence 34, Appl
C 686	9.2	57.5	19	4	US-09-097-239-11	Sequence 11, Appl	C 759	9.2	57.5	26	4	US-09-325-201B-1007	Sequence 1007, Ap
C 687	9.2	57.5	19	4	US-09-474-178-29	Sequence 29, Appl	C 760	9.2	57.5	27	1	US-07-566-278-3	Sequence 3, Appl
C 688	9.2	57.5	20	1	US-08-063-632-1	Sequence 1, Appl	C 761	9.2	57.5	27	1	US-08-590-804-8	Sequence 8, Appl
C 689	9.2	57.5	20	1	US-08-471-724-14	Sequence 14, Appl	C 762	9.2	57.5	27	3	US-09-042-353-3	Sequence 3, Appl
C 690	9.2	57.5	20	2	US-08-471-969-14	Sequence 14, Appl	C 763	9.2	57.5	27	4	US-08-758-413-271	Sequence 271, Appl
C 691	9.2	57.5	20	2	US-08-384-137-14	Sequence 14, Appl	C 764	9.2	57.5	27	4	US-09-020-846-17	Sequence 17, Appl
C 692	9.2	57.5	20	2	US-08-975-211-14	Sequence 14, Appl	C 765	9.2	57.5	28	2	US-08-519-283A-3	Sequence 3, Appl
C 693	9.2	57.5	20	2	US-08-470-006A-14	Sequence 14, Appl	C 766	9.2	57.5	28	2	US-08-788-711-3	Sequence 842, App
C 694	9.2	57.5	20	3	US-08-691-563C-14	Sequence 11, Appl	C 767	9.2	57.5	28	2	US-08-859-998-842	Sequence 131, App
C 695	9.2	57.5	20	3	US-08-914-961-11	Sequence 226, App	C 768	9.2	57.5	28	3	US-08-544-381B-131	Sequence 842, App
C 696	9.2	57.5	20	3	US-09-009-913-226	Sequence 14, Appl	C 769	9.2	57.5	28	4	US-09-225-928-842	Sequence 842, App
C 697	9.2	57.5	20	3	US-09-200-990-14	Sequence 14, Appl	C 770	9.2	57.5	28	4	US-09-225-201B-842	Sequence 37, Appl
C 698	9.2	57.5	20	3	US-09-282-736-14	Sequence 1, Appl	C 771	9.2	57.5	28	4	US-09-438-268-37	Sequence 3, Appl
C 699	9.2	57.5	20	4	US-09-384-749-1	Sequence 2, Appl	C 772	9.2	57.5	29	2	US-08-537-402-3	Sequence 25, Appl
C 700	9.2	57.5	20	4	US-09-555-778-2	Sequence 14, Appl	C 773	9.2	57.5	29	2	US-08-716-317-25	Sequence 13, Appl
C 701	9.2	57.5	20	4	US-09-133-411-14	Sequence 14, Appl	C 774	9.2	57.5	29	2	US-08-232-016-13	Sequence 24, Appl
C 702	9.2	57.5	20	4	US-09-167-109-50	Sequence 14, Appl	C 775	9.2	57.5	30	1	US-08-479-487-24	Sequence 76, App
C 703	9.2	57.5	20	4	US-09-657-452A-90	Sequence 90, Appl	C 776	9.2	57.5	30	1	US-08-647-584-100	Sequence 100, Appl
C 704	9.2	57.5	20	4	US-09-088-274-21	Sequence 5781, Ap	C 777	9.2	57.5	30	2	US-08-544-332-76	Sequence 3, Appl
C 705	9.2	57.5	20	4	US-09-422-978-5781	Sequence 21, Appl	C 778	9.2	57.5	30	3	US-08-852-629-3	Sequence 9, Appl
C 706	9.2	57.5	20	4	US-09-180-570A-17	Sequence 17, Appl	C 779	9.2	57.5	30	3	US-09-321-831-9	Sequence 11, Appl
C 707	9.2	57.5	20	4	US-09-198-452A-2494	Sequence 3232, Ap	C 780	9.2	57.5	30	3	US-09-321-831-11	Sequence 9, Appl
C 708	9.2	57.5	20	4	US-09-198-452A-3222	Sequence 3712, Ap	C 781	9.2	57.5	30	4	US-09-374-038-9	Sequence 9, Appl
C 709	9.2	57.5	20	4	US-09-198-452A-3712	Sequence 5936, Ap	C 782	9.2	57.5	30	4	US-09-370-861A-72	Sequence 72, Appl
C 710	9.2	57.5	20	4	US-09-198-452A-5936	Sequence 2, Appl	C 783	9.2	57.5	30	4	US-09-658-179-9	Sequence 9, Appl
C 711	9.2	57.5	20	4	US-09-649-728-2	Sequence 14, Appl	C 784	9.2	57.5	30	4	US-09-529-279-23	Sequence 23, Appl
C 712	9.2	57.5	20	4	US-09-374-766-14	Sequence 11, Appl	C 785	9.2	57.5	30	4	US-09-538-709-20	Sequence 20, Appl
C 713	9.2	57.5	20	4	US-08-979-847B-14	Sequence 11, Appl	C 786	9.2	57.5	30	4	US-08-948-113D-8	Sequence 8, Appl
C 714	9.2	57.5	21	2	US-08-669-284B-11	Sequence 70, Appl	C 787	9.2	57.5	30	4	US-10-158-895-23	Sequence 23, Appl
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C 716	9.2	57.5	21	3	US-08-368-704C-68	Sequence 15, Appl	C 789	9.2	57.5	31	4	PCT-US95-01944-7	Sequence 7, Appl
C 717	9.2	57.5	22	1	US-08-357-565-15	Sequence 695, App	C 790	9.2	57.5	31	4	US-09-916-510A-16	Sequence 16, Appl
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C 721	9.2	57.5	22	2	US-08-454-720A-13	Sequence 43, Appl	C 794	9.2	57.5	32	2	US-07-673-661B-14	Sequence 107, App
C 722	9.2	57.5	22	3	US-08-867-381A-45	Sequence 260, App	C 795	9.2	57.5	32	3	US-08-783-853A-107	Sequence 8, Appl
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C 725	9.2	57.5	22	4	US-09-521-144-43	Sequence 260, App	C 798	9.2	57.5	32	4	US-08-134-346A-12	Sequence 25, Appl
C 726	9.2	57.5	22	5	PCT-US93-00977-260	Sequence 264, App	C 799	9.2	57.5	32	4	US-08-976-288A-25	Sequence 107, App
C 727	9.2	57.5	22	5	PCT-US93-00977-264	Sequence 2, Appl	C 800	9.2	57.5	32	4	US-09-344-050-10A-14	Sequence 14, Appl
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C 736	9.2	57.5	24	1	US-08-532-390-1	Sequence 53, Appl	C 809	9.2	57.5	33	3	US-09-026-673-5	Sequence 3, Appl
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C 738	9.2	57.5	24	3	US-08-835-728B-157	Sequence 6, Appl	C 811	9.2	57.5	33	4	US-08-479-737-38	Sequence 38, Appl
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C 901	9.2	57.5	47	5	PCT-US93-12388-125	Sequence 125, App	C 974	9.2	57.5	69	5	PCT-US93-09649A-18	Sequence 18, Appl
C 902	9.2	57.5	50	1	US-08-472-194A-19	Sequence 19, Appl	C 975	9.2	57.5	69	5	PCT-US93-09649-18	Sequence 18, Appl
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998 9.2 57.5 79 4 US-10-037-282-7 Sequence 7, Appl
999 9.2 57.5 79 5 PCT-US96-09455A-139 Sequence 139, App
1000 9.2 57.5 79 5 PCT-US96-09455A-165 Sequence 165, App

```

## ALIGNMENTS

```

RESULT 1
US-09-536-393-19
; Sequence 19, Application US/09536393
; Patent No. 6562570
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Scherr, Michaela
; APPLICANT: R1998, Arthur D.
; TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-285
; CURRENT APPLICATION NUMBER: US/09/536,393
; CURRENT FILING DATE: 2000-03-28
; EARLIER APPLICATION NUMBER: 60/127,529
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme core
US-09-536-393-19
Query Match          97.5%; Score 15.6; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 4;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACAACGA 16
Db      1 AGGCTAGCTACAACGA 16

RESULT 2
US-09-536-393-20
; Sequence 20, Application US/09536393
; Patent No. 6562570
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Scherr, Michaela
; APPLICANT: R1998, Arthur D.
; TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-285
; CURRENT APPLICATION NUMBER: US/09/536,393

```

```

; CURRENT FILING DATE: 2000-03-28
; EARLIER APPLICATION NUMBER: 60/127,529
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme core
US-09-536-393-20
Query Match          97.5%; Score 15.6; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 4;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RGGCTAGCTACAACGA 16
Db      1 AGGCTAGCTACAACGA 16

```

```

RESULT 3
US-09-270-140A-23
; Sequence 23, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J61799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: N-ras codon 61 position 1 - mutant (C to A, G or
; OTHER INFORMATION: U)
US-09-270-140A-23
Query Match          97.5%; Score 15.6; DB 4; Length 29;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RGGCTAGCTACAACGA 16
Db      8 AGGCTAGCTACAACGA 23

```

```

RESULT 4
US-09-270-140A-25
; Sequence 25, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J61799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1

```

SEQ ID NO 25  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
OTHER INFORMATION: N-ras codon 61, position 1  
US-09-270-140A-25

Query Match 97.5%; Score 15.6; DB 4; Length 29;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
DB 9 AGGCTAGCTACACGA 24

RESULT 5  
US-09-270-140A-55  
Sequence 55, Application US/09270140A  
Patent No. 6361941  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison  
APPLICANT: Fuery, Caroline  
APPLICANT: Cairns, Murray  
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
FILE REFERENCE: J61799  
CURRENT APPLICATION NUMBER: US/09/270,140A  
CURRENT FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 60/079,651  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 55  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
OTHER INFORMATION: codon 508 - mutant (CTT deletion) for Cystic  
US-09-270-140A-55

Query Match 97.5%; Score 15.6; DB 4; Length 30;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
DB 8 AGGCTAGCTACACGA 23

RESULT 6  
US-09-253-955-5  
Sequence 5, Application US/09253955  
Patent No. 6140055  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison V  
APPLICANT: Fuery, Caroline J  
APPLICANT: Cairns, Murray J  
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
TITLE OF INVENTION: Molecules And Kits  
FILE REFERENCE: J1770SequenceListing  
CURRENT APPLICATION NUMBER: US/09/253,955  
CURRENT FILING DATE: 1999-02-22  
EARLIER APPLICATION NUMBER: 60/076,899  
EARLIER FILING DATE: 1998-03-05  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 31  
TYPE: DNA

ORGANISM: synthetic construct  
US-09-253-955-5

Query Match 97.5%; Score 15.6; DB 3; Length 31;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
DB 8 AGGCTAGCTACACGA 23

RESULT 7  
US-09-637-405-5  
Sequence 5, Application US/09637405  
Patent No. 620113  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison V  
APPLICANT: Fuery, Caroline J  
APPLICANT: Cairns, Murray J  
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
TITLE OF INVENTION: Molecules And Kits  
FILE REFERENCE: J1770SequenceListing  
CURRENT APPLICATION NUMBER: US/09/637,405  
CURRENT FILING DATE: 2000-08-11  
EARLIER APPLICATION NUMBER: 09/253,955  
EARLIER FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 31  
TYPE: DNA  
ORGANISM: synthetic construct  
US-09-637-405-5

Query Match 97.5%; Score 15.6; DB 3; Length 31;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
DB 8 AGGCTAGCTACACGA 23

RESULT 8  
US-09-270-140A-42  
Sequence 42, Application US/09270140A  
Patent No. 6361941  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison  
APPLICANT: Fuery, Caroline  
APPLICANT: Cairns, Murray  
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
FILE REFERENCE: J61799  
CURRENT APPLICATION NUMBER: US/09/270,140A  
CURRENT FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 60/079,651  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
OTHER INFORMATION: codon 542 - Cystic Fibrosis  
US-09-270-140A-42

Query Match 97.5%; Score 15.6; DB 4; Length 31;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
: |||||  
Db 10 AGGCTAGCTACACGA 25

## RESULT 9

US-09-270-140A-45  
; Sequence 45, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Fuary, Allison  
; APPLICANT: Todd, Allison  
; APPLICANT: Fuary, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: J631799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
; OTHER INFORMATION: cystic Fibrosis Codon 542 - mutant (G to U)  
US-09-270-140A-45

Query Match 97.5%; Score 15.6; DB 4; Length 31;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
: |||||  
Db 10 AGGCTAGCTACACGA 25

## RESULT 10

US-09-270-140A-48  
; Sequence 48, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Allison  
; APPLICANT: Fuary, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: J631799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 48  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
; OTHER INFORMATION: Codon 551 - wildtype  
US-09-270-140A-48

Query Match 97.5%; Score 15.6; DB 4; Length 31;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
: |||||  
Db 9 GGGCTAGCTACACGA 24

RESULT 11  
US-09-270-140A-51  
; Sequence 51, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Allison  
; APPLICANT: Fuary, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: J631799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 51  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for  
; OTHER INFORMATION: Codon 51 - mutant (G to A)  
US-09-270-140A-51

Query Match 97.5%; Score 15.6; DB 4; Length 31;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
: |||||  
Db 9 AGGCTAGCTACACGA 24

## RESULT 12

US-09-746-985B-5  
; Sequence 5, Application US/09746985B  
; Patent No. 6365724  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Allison V  
; APPLICANT: Fuary, Caroline J  
; APPLICANT: Cairns, Murray J  
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
; FILE REFERENCE: SequenceListing  
; CURRENT APPLICATION NUMBER: US/09/746,985B  
; CURRENT FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/076,899  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-09-746-985B-5

Query Match 97.5%; Score 15.6; DB 4; Length 31;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
: |||||  
Db 8 AGGCTAGCTACACGA 23

## RESULT 13

US-09-270-140A-12  
; Sequence 12, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:

```

; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; OTHER INFORMATION: H-ras codon 61, position 1-mutant
US-09-270-140A-12

```

```

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  RGCTAGCTACACGA 16
      : |||||
Db      10 GGGCTAGCTACACGA 25

```

```

RESULT 14
US-09-270-140A-15
; Sequence 15, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; OTHER INFORMATION: H-ras codon 61
US-09-270-140A-15

```

```

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  RGCTAGCTACACGA 16
      : |||||
Db      12 GGGCTAGCTACACGA 27

```

```

RESULT 15
US-09-270-140A-19
; Sequence 19, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799

```

```

; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; OTHER INFORMATION: H-ras codon 61, position 3
US-09-270-140A-19

```

```

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  RGCTAGCTACACGA 16
      : |||||
Db      11 AGGCTAGCTACACGA 26

```

```

RESULT 16
US-09-270-140A-28
; Sequence 28, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme
; OTHER INFORMATION: H-ras codon 61
US-09-270-140A-28

```

```

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  RGCTAGCTACACGA 16
      : |||||
Db      9  RGCTAGCTACACGA 24

```

```

RESULT 17
US-09-270-140A-58
; Sequence 58, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1

```

```
; SEQ ID NO 58
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; US-09-270-140A-58

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACACGA 16
       :|||||
Db      9 GGGCTAGCTACACGA 24

RESULT 18
US-09-270-140A-9
; Sequence 9, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc01799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; US-09-270-140A-9

Query Match          97.5%; Score 15.6; DB 4; Length 34;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACACGA 16
       :|||||
Db     13 AGGCTAGCTACACGA 28

RESULT 19
US-09-270-140A-53
; Sequence 53, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc01799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 53
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; US-09-270-140A-53
; OTHER INFORMATION: codon 08 - wildtype

Query Match          97.5%; Score 15.6; DB 4; Length 34;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACACGA 16
       :|||||
Db     11 AGGCTAGCTACACGA 26

RESULT 20
US-09-270-140A-3
; Sequence 3, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc01799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; US-09-270-140A-3

Query Match          97.5%; Score 15.6; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACACGA 16
       :|||||
Db     11 RGGCTAGCTACACGA 26

RESULT 21
US-09-270-140A-6
; Sequence 6, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc01799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme
; US-09-270-140A-6

Query Match          97.5%; Score 15.6; DB 4; Length 35;
Best Local Similarity 93.8%; Pred. No. 4.2;
```

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
:|||||  
Db 11 AGGCTAGCTACACGA 26

## RESULT 22

US-09-270-140A-31  
; Sequence 31, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Puery, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: Jc11799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for  
; OTHER INFORMATION: Codon 70 HIV-1 AZT resistant mutant  
US-09-270-140A-31

Query Match 97.5%; Score 15.6; DB 4; Length 35;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
:|||||  
Db 9 AGGCTAGCTACACGA 24

## RESULT 23

US-09-270-140A-39  
; Sequence 39, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Puery, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: Jc11799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for  
; OTHER INFORMATION: codon 74  
US-09-270-140A-39

Query Match 97.5%; Score 15.6; DB 4; Length 35;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
:|||||  
Db 8 AGGCTAGCTACACGA 23

RESULT 24  
US-09-270-140A-34  
; Sequence 34, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Puery, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: Jc11799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for  
; OTHER INFORMATION: codon 215 - mutant (C to U or A)  
US-09-270-140A-34

Query Match 97.5%; Score 15.6; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
:|||||  
Db 11 AGGCTAGCTACACGA 26

## RESULT 25

US-09-270-140A-36  
; Sequence 36, Application US/09270140A  
; Patent No. 6361941  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison  
; APPLICANT: Puery, Caroline  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: Jc11799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for  
; OTHER INFORMATION: codon 215 - mutant  
US-09-270-140A-36

Query Match 97.5%; Score 15.6; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 4.2;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
:|||||  
Db 10 GGGCTAGCTACACGA 25

## RESULT 26

US-09-270-140A-91  
; Sequence 91, Application US/09270140A

```
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: Jc11799
CURRENT APPLICATION NUMBER: US/09/270,140A
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 91
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: D21 DNazyme
US-09-270-140A-91

Query Match          97.5%; Score 15.6; DB 4; Length 39;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACAACGA 16
      : |||||
      8 GGGCTAGCTACAACGA 23

RESULT 27
US-09-270-140A-94
Sequence 94, Application US/09270140A
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: Jc11799
CURRENT APPLICATION NUMBER: US/09/270,140A
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 94
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: D23 DNazyme
US-09-270-140A-94

Query Match          97.5%; Score 15.6; DB 4; Length 39;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACAACGA 16
      : |||||
      8 AGGCTAGCTACAACGA 23

RESULT 28
US-08-849-567A-85
Sequence 85, Application US/08849567A
Patent No. 6326174
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald F.
APPLICANT: Breaker, Ronald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REFERENCE: SCR19435
CURRENT APPLICATION NUMBER: US/08/849,567A
```

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CURRENT FILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: PCT/US95/15580
PRIOR FILING DATE: 1995-12-01
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/349,023
PRIOR FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 85
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-85

Query Match          97.5%; Score 15.6; DB 4; Length 47;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACAACGA 16
      : |||||
      11 AGGCTAGCTACAACGA 26

RESULT 29
US-08-849-567A-87
Sequence 87, Application US/08849567A
Patent No. 6326174
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald F.
APPLICANT: Breaker, Ronald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REFERENCE: SCR19435
CURRENT APPLICATION NUMBER: US/08/849,567A
PRIOR FILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: PCT/US95/15580
PRIOR FILING DATE: 1995-12-01
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/349,023
PRIOR FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 87
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-87

Query Match          97.5%; Score 15.6; DB 4; Length 48;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCTACAACGA 16
      : |||||
      10 AGGCTAGCTACAACGA 25

RESULT 30
US-08-849-567A-81
Sequence 81, Application US/08849567A
Patent No. 6326174
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald F.
APPLICANT: Breaker, Ronald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REFERENCE: SCR19435
CURRENT APPLICATION NUMBER: US/08/849,567A
```

```
;; PRIOR APPLICATION NUMBER: PCT/US95/15580
;; PRIOR FILING DATE: 1995-12-01
;; PRIOR APPLICATION NUMBER: 08/472,194
;; PRIOR FILING DATE: 1995-06-07
;; PRIOR APPLICATION NUMBER: 08/349,023
;; PRIOR FILING DATE: 1994-12-02
;; NUMBER OF SEQ ID NOS: 101
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 81
;; LENGTH: 49
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-81

Query Match          97.5%; Score 15.6; DB 4; Length 49;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCGTAGCTACAACGA 16
Db      10 AGGCTAGCTACAACGA 25
      :|||||
      :|||||

RESULT 31
US-09-253-955-8/c
; Sequence 8, Application US/09253955
; Patent No. 6140055
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; FILE REFERENCE: J01770SequenceListing
; CURRENT APPLICATION NUMBER: US/09/253,955
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,899
; EARLIER FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-253-955-8

Query Match          97.5%; Score 15.6; DB 3; Length 50;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCGTAGCTACAACGA 16
Db      22 AGGCTAGCTACAACGA 7
      :|||||
      :|||||

RESULT 32
US-09-637-405-8/c
; Sequence 8, Application US/09637405
; Patent No. 6201113
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; FILE REFERENCE: J01770SequenceListing
; CURRENT APPLICATION NUMBER: US/09/637,405
; CURRENT FILING DATE: 2000-08-11
; EARLIER APPLICATION NUMBER: 09/253,955
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 11
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;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 8
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: synthetic construct
US-09-637-405-8

Query Match          97.5%; Score 15.6; DB 3; Length 50;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCGTAGCTACAACGA 16
Db      22 AGGCTAGCTACAACGA 7
      :|||||
      :|||||

RESULT 33
US-09-746-985B-8/c
; Sequence 8, Application US/09746985B
; Patent No. 6365724
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; FILE REFERENCE: SequenceListing
; CURRENT APPLICATION NUMBER: US/09/746,985B
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/076,899
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-746-985B-8

Query Match          97.5%; Score 15.6; DB 4; Length 50;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCGTAGCTACAACGA 16
Db      22 AGGCTAGCTACAACGA 7
      :|||||
      :|||||

RESULT 34
US-08-849-567A-86
; Sequence 86, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
; FILE REFERENCE: SCR19435
; CURRENT APPLICATION NUMBER: US/08/849,567A
; CURRENT FILING DATE: 1997-08-25
; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
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FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme  
US-08-849-567A-86

Query Match 97.5%; Score 15.6; DB 4; Length 51;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
:|||||  
DB 11 AGGCTAGCTACACGA 26

RESULT 35  
US-09-253-955-2/c  
Sequence 2, Application US/09253955  
Patent No. 6140055  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison V  
APPLICANT: Fuery, Caroline J  
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
FILE REFERENCE: J1170SequenceListing  
CURRENT APPLICATION NUMBER: US/09/253,955  
CURRENT FILING DATE: 1999-02-22  
EARLIER APPLICATION NUMBER: 60/076,899  
EARLIER FILING DATE: 1998-03-05  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 59  
TYPE: DNA  
ORGANISM: synthetic construct  
US-09-253-955-2

Query Match 97.5%; Score 15.6; DB 3; Length 59;  
Best Local Similarity 93.8%; Pred. No. 4.4;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
:|||||  
DB 28 AGGCTAGCTACACGA 13

RESULT 36  
US-09-637-405-2/c  
Sequence 2, Application US/09637405  
Patent No. 6201113  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison V  
APPLICANT: Fuery, Caroline J  
APPLICANT: Cairns, Murray J  
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
FILE REFERENCE: J1170SequenceListing  
CURRENT APPLICATION NUMBER: US/09/637,405  
CURRENT FILING DATE: 2000-08-11  
EARLIER APPLICATION NUMBER: 09/253,955  
EARLIER FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 59  
TYPE: DNA  
ORGANISM: synthetic construct  
US-09-637-405-2

Query Match 97.5%; Score 15.6; DB 3; Length 59;  
Best Local Similarity 93.8%; Pred. No. 4.4;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16

DB 28 AGGCTAGCTACACGA 13  
:|||||

RESULT 37  
US-09-746-985B-2/c  
Sequence 2, Application US/09746985B  
Patent No. 6365724  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison V  
APPLICANT: Fuery, Caroline J  
APPLICANT: Cairns, Murray J  
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
FILE REFERENCE: SequenceListing  
CURRENT APPLICATION NUMBER: US/09/746,985B  
CURRENT FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: 60/076,899  
PRIOR FILING DATE: 1998-03-05  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 59  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR primer  
US-09-746-985B-2

Query Match 97.5%; Score 15.6; DB 4; Length 59;  
Best Local Similarity 93.8%; Pred. No. 4.4;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
:|||||  
DB 28 AGGCTAGCTACACGA 13

RESULT 38  
US-09-253-955-10/c  
Sequence 10, Application US/09253955  
Patent No. 6140055  
GENERAL INFORMATION:  
APPLICANT: Todd, Alison V  
APPLICANT: Fuery, Caroline J  
APPLICANT: Cairns, Murray J  
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
FILE REFERENCE: J1170SequenceListing  
CURRENT APPLICATION NUMBER: US/09/253,955  
CURRENT FILING DATE: 1999-02-22  
EARLIER APPLICATION NUMBER: 60/076,899  
EARLIER FILING DATE: 1998-03-05  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 60  
TYPE: DNA  
ORGANISM: synthetic construct  
US-09-253-955-10

Query Match 97.5%; Score 15.6; DB 3; Length 60;  
Best Local Similarity 93.8%; Pred. No. 4.4;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
:|||||  
DB 32 GGGCTAGCTACACGA 17

RESULT 39  
US-09-637-405-10/c  
Sequence 10, Application US/09637405

; Patent No. 620113  
; GENERAL INFORMATION:  
; APPLICANT: Todd, Alison V  
; APPLICANT: Fuery, Caroline J  
; APPLICANT: Cairns, Murray J  
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related  
; TITLE OF INVENTION: Molecules And Kits  
; FILE REFERENCE: j1170SequenceListing  
; CURRENT APPLICATION NUMBER: US/09/637,405  
; CURRENT FILING DATE: 2000-08-11  
; EARLIER APPLICATION NUMBER: 09/253,955  
; EARLIER FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-637-405-10

Query Match 97.5%; Score 15.6; DB 3; Length 60;  
Best Local Similarity 93.8%; Pred. No. 4.4;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
: |||||  
Db 32 GGGCTAGCTACACGA 17

RESULT 40  
US-09-270-140A-95/c  
; Sequence 95, Application US/09270140A  
; Patent No. 6361941

; GENERAL INFORMATION:  
; APPLICANT: Fuery, Allison  
; APPLICANT: Todd, Alison  
; APPLICANT: Cairns, Murray  
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods  
; FILE REFERENCE: J411799  
; CURRENT APPLICATION NUMBER: US/09/270,140A  
; CURRENT FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 60/079,651  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: 3' zymogene  
; OTHER INFORMATION: primer ek42b22  
US-09-270-140A-95

Query Match 97.5%; Score 15.6; DB 4; Length 60;  
Best Local Similarity 93.8%; Pred. No. 4.4;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16  
: |||||  
Db 32 GGGCTAGCTACACGA 17

Search completed: January 21, 2004, 08:17:05  
Job time : 60 secs

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OM nucleic - nucleic search, using sw model1

Run on: January 21, 2004, 06:47:52 : Search time 154 Seconds  
(without alignments)  
366.209 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16

Sequence: 1 rgcgtagctacacga 16

Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 1462038

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	97.5	16	10	US-09-877-526A-21
2	15.6	97.5	16	10	US-09-866-116B-15
3	15.6	97.5	16	10	US-09-864-785-3928
4	15.6	97.5	16	11	US-09-992-160-21
5	15.6	97.5	16	11	US-09-730-289B-3896
6	15.6	97.5	16	11	US-09-780-533A-6679
7	15.6	97.5	16	11	US-09-877-478-6585
8	15.6	97.5	16	11	US-09-848-754A-9645
9	15.6	97.5	16	11	US-09-776-474-2991
10	15.6	97.5	16	11	US-09-930-423-4545
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91	15.6	97.5	29	12	US-10-420-194-779	Sequence 779, App	164	15.6	97.5	30	13	US-09-817-879-9599	Sequence 9599, App
92	15.6	97.5	29	12	US-10-420-194-781	Sequence 781, App	165	15.6	97.5	30	13	US-09-817-879-9599	Sequence 9599, App
93	15.6	97.5	29	12	US-10-420-194-786	Sequence 786, App	166	15.6	97.5	30	13	US-09-817-879-9600	Sequence 9600, App
94	15.6	97.5	29	12	US-10-420-194-788	Sequence 788, App	167	15.6	97.5	30	13	US-09-817-879-9601	Sequence 9601, App
95	15.6	97.5	29	12	US-10-420-194-792	Sequence 792, App	168	15.6	97.5	30	13	US-09-817-879-9602	Sequence 9602, App
96	15.6	97.5	29	12	US-10-420-194-795	Sequence 795, App	169	15.6	97.5	30	13	US-09-817-879-9603	Sequence 9603, App
97	15.6	97.5	29	12	US-10-420-194-799	Sequence 799, App	170	15.6	97.5	30	13	US-09-817-879-9604	Sequence 9604, App
98	15.6	97.5	29	12	US-10-420-194-804	Sequence 804, App	171	15.6	97.5	30	13	US-09-817-879-9605	Sequence 9605, App
99	15.6	97.5	29	13	US-10-277-494-302	Sequence 302, App	172	15.6	97.5	30	13	US-09-817-879-9606	Sequence 9606, App
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102	15.6	97.5	29	13	US-10-277-494-305	Sequence 305, App	175	15.6	97.5	30	15	US-10-163-552-1985	Sequence 1985, App
103	15.6	97.5	29	13	US-10-277-494-306	Sequence 306, App	176	15.6	97.5	30	15	US-10-163-552-1986	Sequence 1986, App
104	15.6	97.5	29	13	US-10-277-494-307	Sequence 307, App	177	15.6	97.5	30	15	US-10-156-306-7919	Sequence 7919, App
105	15.6	97.5	29	13	US-10-277-494-308	Sequence 308, App	178	15.6	97.5	30	15	US-10-156-306-7920	Sequence 7920, App
106	15.6	97.5	29	13	US-10-277-494-309	Sequence 309, App	179	15.6	97.5	30	15	US-10-156-306-7921	Sequence 7921, App
107	15.6	97.5	29	13	US-10-277-494-310	Sequence 310, App	180	15.6	97.5	30	15	US-10-156-306-7922	Sequence 7922, App
108	15.6	97.5	29	13	US-10-277-494-311	Sequence 311, App	181	15.6	97.5	30	15	US-10-156-306-7923	Sequence 7923, App
109	15.6	97.5	29	13	US-10-277-494-312	Sequence 312, App	182	15.6	97.5	30	15	US-10-156-306-7924	Sequence 7924, App
110	15.6	97.5	29	13	US-10-277-494-313	Sequence 313, App	183	15.6	97.5	30	15	US-10-156-306-7925	Sequence 7925, App
111	15.6	97.5	29	13	US-10-277-494-314	Sequence 314, App	184	15.6	97.5	30	15	US-10-156-306-7926	Sequence 7926, App
112	15.6	97.5	29	13	US-10-277-494-315	Sequence 315, App	185	15.6	97.5	30	15	US-10-156-306-7927	Sequence 7927, App
113	15.6	97.5	29	13	US-10-277-494-316	Sequence 316, App	186	15.6	97.5	30	15	US-10-156-306-7928	Sequence 7928, App
114	15.6	97.5	29	13	US-10-277-494-317	Sequence 317, App	187	15.6	97.5	31	9	US-09-813-380-0	Sequence 9, Appl
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116	15.6	97.5	29	13	US-10-277-494-319	Sequence 319, App	189	15.6	97.5	31	10	US-09-864-785-2152	Sequence 2152, App
117	15.6	97.5	29	13	US-10-277-494-320	Sequence 320, App	190	15.6	97.5	31	10	US-09-864-785-2153	Sequence 2153, App
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119	15.6	97.5	29	15	US-10-122-013-3	Sequence 3, Appl	192	15.6	97.5	31	10	US-09-864-785-2155	Sequence 2155, App
120	15.6	97.5	29	15	US-10-122-013-4	Sequence 4, Appl	193	15.6	97.5	31	10	US-09-864-785-2156	Sequence 2156, App
121	15.6	97.5	29	15	US-10-122-013-5	Sequence 5, Appl	194	15.6	97.5	31	10	US-09-864-785-2157	Sequence 2157, App
122	15.6	97.5	29	15	US-10-122-013-6	Sequence 6, Appl	195	15.6	97.5	31	10	US-09-864-785-2158	Sequence 2158, App
123	15.6	97.5	29	15	US-10-122-013-7	Sequence 7, Appl	196	15.6	97.5	31	10	US-09-864-785-2159	Sequence 2159, App
124	15.6	97.5	29	15	US-10-122-013-8	Sequence 8, Appl	197	15.6	97.5	31	10	US-09-864-785-2160	Sequence 2160, App
125	15.6	97.5	29	15	US-10-122-013-9	Sequence 9, Appl	198	15.6	97.5	31	10	US-09-864-785-2161	Sequence 2161, App
126	15.6	97.5	29	15	US-10-122-013-10	Sequence 10, Appl	199	15.6	97.5	31	10	US-09-864-785-2162	Sequence 2162, App
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128	15.6	97.5	29	15	US-10-122-013-12	Sequence 12, Appl	201	15.6	97.5	31	10	US-09-864-785-2164	Sequence 2164, App
129	15.6	97.5	29	15	US-10-122-013-13	Sequence 13, Appl	202	15.6	97.5	31	10	US-09-864-785-2165	Sequence 2165, App
130	15.6	97.5	29	15	US-10-122-013-14	Sequence 14, Appl	203	15.6	97.5	31	10	US-09-864-785-2166	Sequence 2166, App
131	15.6	97.5	29	15	US-10-122-013-15	Sequence 15, Appl	204	15.6	97.5	31	10	US-09-864-785-2167	Sequence 2167, App
132	15.6	97.5	29	15	US-10-122-013-16	Sequence 16, Appl	205	15.6	97.5	31	10	US-09-864-785-2168	Sequence 2168, App
133	15.6	97.5	29	15	US-10-157-580A-149	Sequence 149, App	206	15.6	97.5	31	10	US-09-864-785-2169	Sequence 2169, App
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135	15.6	97.5	29	15	US-10-157-580A-151	Sequence 151, App	208	15.6	97.5	31	10	US-09-864-785-2171	Sequence 2171, App
136	15.6	97.5	29	15	US-10-157-580A-152	Sequence 152, App	209	15.6	97.5	31	10	US-09-864-785-2172	Sequence 2172, App
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138	15.6	97.5	30	10	US-09-864-785-3909	Sequence 3909, App	211	15.6	97.5	31	10	US-09-864-785-2174	Sequence 2174, App
139	15.6	97.5	30	10	US-09-864-785-3910	Sequence 3910, App	212	15.6	97.5	31	10	US-09-864-785-2175	Sequence 2175, App
140	15.6	97.5	30	10	US-09-864-785-3911	Sequence 3911, App	213	15.6	97.5	31	10	US-09-864-785-2176	Sequence 2176, App
141	15.6	97.5	30	10	US-09-864-785-3912	Sequence 3912, App	214	15.6	97.5	31	10	US-09-864-785-2177	Sequence 2177, App
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144	15.6	97.5	30	11	US-09-877-478-6568	Sequence 6568, App	217	15.6	97.5	31	10	US-09-864-785-2180	Sequence 2180, App
145	15.6	97.5	30	11	US-09-877-478-6569	Sequence 6569, App	218	15.6	97.5	31	10	US-09-864-785-2181	Sequence 2181, App
146	15.6	97.5	30	11	US-09-877-478-6570	Sequence 6570, App	219	15.6	97.5	31	10	US-09-864-785-2182	Sequence 2182, App
147	15.6	97.5	30	11	US-09-877-478-6571	Sequence 6571, App	220	15.6	97.5	31	10	US-09-864-785-2183	Sequence 2183, App
148	15.6	97.5	30	11	US-09-740-332-9597	Sequence 9597, App	221	15.6	97.5	31	10	US-09-864-785-2184	Sequence 2184, App
149	15.6	97.5	30	11	US-09-740-332-9598	Sequence 9598, App	222	15.6	97.5	31	10	US-09-864-785-2185	Sequence 2185, App
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156	15.6	97.5	30	11	US-09-740-332-9605	Sequence 9605, App	229	15.6	97.5	31	10	US-09-864-785-2192	Sequence 2192, App
157	15.6	97.5	30	11	US-09-740-332-9606	Sequence 9606, App	230	15.6	97.5	31	10	US-09-864-785-2193	Sequence 2193, App
158	15.6	97.5	30	13	US-09-792-818-2287	Sequence 2287, App	231	15.6	97.5	31	10	US-09-864-785-2194	Sequence 2194, App
159	15.6	97.5	30	13	US-09-792-818-2288	Sequence 2288, App	232	15.6	97.5	31	10	US-09-864-785-2195	Sequence 2195, App
160	15.6	97.5	30	13	US-09-792-818-2289	Sequence 2289, App	233	15.6	97.5	31	10	US-09-864-785-2196	Sequence 2196, App
161	15.6	97.5	30	13	US-09-792-818-2290	Sequence 2290, App	234	15.6	97.5	31	10	US-09-864-785-2197	Sequence 2197, App

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239	15.6	97.5	31	10	US-09-864-785-2202	Sequence 2202, Ap	312	15.6	97.5	31	10	US-09-864-785-2275	Sequence 2275, Ap
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244	15.6	97.5	31	10	US-09-864-785-2207	Sequence 2207, Ap	317	15.6	97.5	31	10	US-09-864-785-2280	Sequence 2280, Ap
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247	15.6	97.5	31	10	US-09-864-785-2210	Sequence 2210, Ap	320	15.6	97.5	31	10	US-09-864-785-2283	Sequence 2283, Ap
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249	15.6	97.5	31	10	US-09-864-785-2212	Sequence 2212, Ap	322	15.6	97.5	31	10	US-09-864-785-2285	Sequence 2285, Ap
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251	15.6	97.5	31	10	US-09-864-785-2214	Sequence 2214, Ap	324	15.6	97.5	31	10	US-09-864-785-2287	Sequence 2287, Ap
252	15.6	97.5	31	10	US-09-864-785-2215	Sequence 2215, Ap	325	15.6	97.5	31	10	US-09-864-785-2288	Sequence 2288, Ap
253	15.6	97.5	31	10	US-09-864-785-2216	Sequence 2216, Ap	326	15.6	97.5	31	10	US-09-864-785-2289	Sequence 2289, Ap
254	15.6	97.5	31	10	US-09-864-785-2217	Sequence 2217, Ap	327	15.6	97.5	31	10	US-09-864-785-2290	Sequence 2290, Ap
255	15.6	97.5	31	10	US-09-864-785-2218	Sequence 2218, Ap	328	15.6	97.5	31	10	US-09-864-785-2291	Sequence 2291, Ap
256	15.6	97.5	31	10	US-09-864-785-2219	Sequence 2219, Ap	329	15.6	97.5	31	10	US-09-864-785-2292	Sequence 2292, Ap
257	15.6	97.5	31	10	US-09-864-785-2220	Sequence 2220, Ap	330	15.6	97.5	31	10	US-09-864-785-2293	Sequence 2293, Ap
258	15.6	97.5	31	10	US-09-864-785-2221	Sequence 2221, Ap	331	15.6	97.5	31	10	US-09-864-785-2294	Sequence 2294, Ap
259	15.6	97.5	31	10	US-09-864-785-2222	Sequence 2222, Ap	332	15.6	97.5	31	10	US-09-864-785-2295	Sequence 2295, Ap
260	15.6	97.5	31	10	US-09-864-785-2223	Sequence 2223, Ap	333	15.6	97.5	31	10	US-09-864-785-2296	Sequence 2296, Ap
261	15.6	97.5	31	10	US-09-864-785-2224	Sequence 2224, Ap	334	15.6	97.5	31	10	US-09-864-785-2297	Sequence 2297, Ap
262	15.6	97.5	31	10	US-09-864-785-2225	Sequence 2225, Ap	335	15.6	97.5	31	10	US-09-864-785-2298	Sequence 2298, Ap
263	15.6	97.5	31	10	US-09-864-785-2226	Sequence 2226, Ap	336	15.6	97.5	31	10	US-09-864-785-2299	Sequence 2299, Ap
264	15.6	97.5	31	10	US-09-864-785-2227	Sequence 2227, Ap	337	15.6	97.5	31	10	US-09-864-785-2300	Sequence 2300, Ap
265	15.6	97.5	31	10	US-09-864-785-2228	Sequence 2228, Ap	338	15.6	97.5	31	10	US-09-864-785-2301	Sequence 2301, Ap
266	15.6	97.5	31	10	US-09-864-785-2229	Sequence 2229, Ap	339	15.6	97.5	31	10	US-09-864-785-2302	Sequence 2302, Ap
267	15.6	97.5	31	10	US-09-864-785-2230	Sequence 2230, Ap	340	15.6	97.5	31	10	US-09-864-785-2303	Sequence 2303, Ap
268	15.6	97.5	31	10	US-09-864-785-2231	Sequence 2231, Ap	341	15.6	97.5	31	10	US-09-864-785-2304	Sequence 2304, Ap
269	15.6	97.5	31	10	US-09-864-785-2232	Sequence 2232, Ap	342	15.6	97.5	31	10	US-09-864-785-2305	Sequence 2305, Ap
270	15.6	97.5	31	10	US-09-864-785-2233	Sequence 2233, Ap	343	15.6	97.5	31	10	US-09-864-785-2306	Sequence 2306, Ap
271	15.6	97.5	31	10	US-09-864-785-2234	Sequence 2234, Ap	344	15.6	97.5	31	10	US-09-864-785-2307	Sequence 2307, Ap
272	15.6	97.5	31	10	US-09-864-785-2235	Sequence 2235, Ap	345	15.6	97.5	31	10	US-09-864-785-2308	Sequence 2308, Ap
273	15.6	97.5	31	10	US-09-864-785-2236	Sequence 2236, Ap	346	15.6	97.5	31	10	US-09-864-785-2309	Sequence 2309, Ap
274	15.6	97.5	31	10	US-09-864-785-2237	Sequence 2237, Ap	347	15.6	97.5	31	10	US-09-864-785-2310	Sequence 2310, Ap
275	15.6	97.5	31	10	US-09-864-785-2238	Sequence 2238, Ap	348	15.6	97.5	31	10	US-09-864-785-2311	Sequence 2311, Ap
276	15.6	97.5	31	10	US-09-864-785-2239	Sequence 2239, Ap	349	15.6	97.5	31	10	US-09-864-785-2312	Sequence 2312, Ap
277	15.6	97.5	31	10	US-09-864-785-2240	Sequence 2240, Ap	350	15.6	97.5	31	10	US-09-864-785-2313	Sequence 2313, Ap
278	15.6	97.5	31	10	US-09-864-785-2241	Sequence 2241, Ap	351	15.6	97.5	31	10	US-09-864-785-2314	Sequence 2314, Ap
279	15.6	97.5	31	10	US-09-864-785-2242	Sequence 2242, Ap	352	15.6	97.5	31	10	US-09-864-785-2315	Sequence 2315, Ap
280	15.6	97.5	31	10	US-09-864-785-2243	Sequence 2243, Ap	353	15.6	97.5	31	10	US-09-864-785-2316	Sequence 2316, Ap
281	15.6	97.5	31	10	US-09-864-785-2244	Sequence 2244, Ap	354	15.6	97.5	31	10	US-09-864-785-2317	Sequence 2317, Ap
282	15.6	97.5	31	10	US-09-864-785-2245	Sequence 2245, Ap	355	15.6	97.5	31	10	US-09-864-785-2318	Sequence 2318, Ap
283	15.6	97.5	31	10	US-09-864-785-2246	Sequence 2246, Ap	356	15.6	97.5	31	10	US-09-864-785-2319	Sequence 2319, Ap
284	15.6	97.5	31	10	US-09-864-785-2247	Sequence 2247, Ap	357	15.6	97.5	31	10	US-09-864-785-2320	Sequence 2320, Ap
285	15.6	97.5	31	10	US-09-864-785-2248	Sequence 2248, Ap	358	15.6	97.5	31	10	US-09-864-785-2321	Sequence 2321, Ap
286	15.6	97.5	31	10	US-09-864-785-2249	Sequence 2249, Ap	359	15.6	97.5	31	10	US-09-864-785-2322	Sequence 2322, Ap
287	15.6	97.5	31	10	US-09-864-785-2250	Sequence 2250, Ap	360	15.6	97.5	31	10	US-09-864-785-2323	Sequence 2323, Ap
288	15.6	97.5	31	10	US-09-864-785-2251	Sequence 2251, Ap	361	15.6	97.5	31	10	US-09-864-785-2324	Sequence 2324, Ap
289	15.6	97.5	31	10	US-09-864-785-2252	Sequence 2252, Ap	362	15.6	97.5	31	10	US-09-864-785-2325	Sequence 2325, Ap
290	15.6	97.5	31	10	US-09-864-785-2253	Sequence 2253, Ap	363	15.6	97.5	31	10	US-09-864-785-2326	Sequence 2326, Ap
291	15.6	97.5	31	10	US-09-864-785-2254	Sequence 2254, Ap	364	15.6	97.5	31	10	US-09-864-785-2327	Sequence 2327, Ap
292	15.6	97.5	31	10	US-09-864-785-2255	Sequence 2255, Ap	365	15.6	97.5	31	10	US-09-864-785-2328	Sequence 2328, Ap
293	15.6	97.5	31	10	US-09-864-785-2256	Sequence 2256, Ap	366	15.6	97.5	31	10	US-09-864-785-2329	Sequence 2329, Ap
294	15.6	97.5	31	10	US-09-864-785-2257	Sequence 2257, Ap	367	15.6	97.5	31	10	US-09-864-785-2330	Sequence 2330, Ap
295	15.6	97.5	31	10	US-09-864-785-2258	Sequence 2258, Ap	368	15.6	97.5	31	10	US-09-864-785-2331	Sequence 2331, Ap
296	15.6	97.5	31	10	US-09-864-785-2259	Sequence 2259, Ap	369	15.6	97.5	31	10	US-09-864-785-2332	Sequence 2332, Ap
297	15.6	97.5	31	10	US-09-864-785-2260	Sequence 2260, Ap	370	15.6	97.5	31	10	US-09-864-785-2333	Sequence 2333, Ap
298	15.6	97.5	31	10	US-09-864-785-2261	Sequence 2261, Ap	371	15.6	97.5	31	10	US-09-864-785-2334	Sequence 2334, Ap
299	15.6	97.5	31	10	US-09-864-785-2262	Sequence 2262, Ap	372	15.6	97.5	31	10	US-09-864-785-2335	Sequence 2335, Ap
300	15.6	97.5	31	10	US-09-864-785-2263	Sequence 2263, Ap	373	15.6	97.5	31	10	US-09-864-785-2336	Sequence 2336, Ap
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302	15.6	97.5	31	10	US-09-864-785-2265	Sequence 2265, Ap	375	15.6	97.5	31	10	US-09-864-785-2338	Sequence 2338, Ap
303	15.6	97.5	31	10	US-09-864-785-2266	Sequence 2266, Ap	376	15.6	97.5	31	10	US-09-864-785-2339	Sequence 2339, Ap
304	15.6	97.5	31	10	US-09-864-785-2267	Sequence 2267, Ap	377	15.6	97.5	31	10	US-09-864-785-2340	Sequence 2340, Ap
305	15.6	97.5	31	10	US-09-864-785-2268	Sequence 2268, Ap	378	15.6	97.5	31	10	US-09-864-785-2341	Sequence 2341, Ap
306	15.6	97.5	31	10	US-09-864-785-2269	Sequence 2269, Ap	379	15.6	97.5	31	10	US-09-864-785-2342	Sequence 2342, Ap
307	15.6	97.5	31	10	US-09-864-785-2270	Sequence 2270, Ap	380	15.6	97.5	31	10	US-09-864-785-2343	Sequence 2343, Ap

381	15.6	97.5	31	10	US-09-864-785-2344	Sequence 2344, Ap	454	15.6	97.5	31	10	US-09-864-785-2417	Sequence 2417, Ap
382	15.6	97.5	31	10	US-09-864-785-2345	Sequence 2345, Ap	455	15.6	97.5	31	10	US-09-864-785-2418	Sequence 2418, Ap
383	15.6	97.5	31	10	US-09-864-785-2346	Sequence 2346, Ap	456	15.6	97.5	31	10	US-09-864-785-2419	Sequence 2419, Ap
384	15.6	97.5	31	10	US-09-864-785-2347	Sequence 2347, Ap	457	15.6	97.5	31	10	US-09-864-785-2420	Sequence 2420, Ap
385	15.6	97.5	31	10	US-09-864-785-2348	Sequence 2348, Ap	458	15.6	97.5	31	10	US-09-864-785-2421	Sequence 2421, Ap
386	15.6	97.5	31	10	US-09-864-785-2349	Sequence 2349, Ap	459	15.6	97.5	31	10	US-09-864-785-2422	Sequence 2422, Ap
387	15.6	97.5	31	10	US-09-864-785-2350	Sequence 2350, Ap	460	15.6	97.5	31	10	US-09-864-785-2423	Sequence 2423, Ap
388	15.6	97.5	31	10	US-09-864-785-2351	Sequence 2351, Ap	461	15.6	97.5	31	10	US-09-864-785-2424	Sequence 2424, Ap
389	15.6	97.5	31	10	US-09-864-785-2352	Sequence 2352, Ap	462	15.6	97.5	31	10	US-09-864-785-2425	Sequence 2425, Ap
390	15.6	97.5	31	10	US-09-864-785-2353	Sequence 2353, Ap	463	15.6	97.5	31	10	US-09-864-785-2426	Sequence 2426, Ap
391	15.6	97.5	31	10	US-09-864-785-2354	Sequence 2354, Ap	464	15.6	97.5	31	10	US-09-864-785-2427	Sequence 2427, Ap
392	15.6	97.5	31	10	US-09-864-785-2355	Sequence 2355, Ap	465	15.6	97.5	31	10	US-09-864-785-2428	Sequence 2428, Ap
393	15.6	97.5	31	10	US-09-864-785-2356	Sequence 2356, Ap	466	15.6	97.5	31	10	US-09-864-785-2429	Sequence 2429, Ap
394	15.6	97.5	31	10	US-09-864-785-2357	Sequence 2357, Ap	467	15.6	97.5	31	10	US-09-864-785-2430	Sequence 2430, Ap
395	15.6	97.5	31	10	US-09-864-785-2358	Sequence 2358, Ap	468	15.6	97.5	31	10	US-09-864-785-2431	Sequence 2431, Ap
396	15.6	97.5	31	10	US-09-864-785-2359	Sequence 2359, Ap	469	15.6	97.5	31	10	US-09-864-785-2432	Sequence 2432, Ap
397	15.6	97.5	31	10	US-09-864-785-2360	Sequence 2360, Ap	470	15.6	97.5	31	10	US-09-864-785-2433	Sequence 2433, Ap
398	15.6	97.5	31	10	US-09-864-785-2361	Sequence 2361, Ap	471	15.6	97.5	31	10	US-09-864-785-2434	Sequence 2434, Ap
399	15.6	97.5	31	10	US-09-864-785-2362	Sequence 2362, Ap	472	15.6	97.5	31	10	US-09-864-785-2435	Sequence 2435, Ap
400	15.6	97.5	31	10	US-09-864-785-2363	Sequence 2363, Ap	473	15.6	97.5	31	10	US-09-864-785-2436	Sequence 2436, Ap
401	15.6	97.5	31	10	US-09-864-785-2364	Sequence 2364, Ap	474	15.6	97.5	31	10	US-09-864-785-2437	Sequence 2437, Ap
402	15.6	97.5	31	10	US-09-864-785-2365	Sequence 2365, Ap	475	15.6	97.5	31	10	US-09-864-785-2438	Sequence 2438, Ap
403	15.6	97.5	31	10	US-09-864-785-2366	Sequence 2366, Ap	476	15.6	97.5	31	10	US-09-864-785-2439	Sequence 2439, Ap
404	15.6	97.5	31	10	US-09-864-785-2367	Sequence 2367, Ap	477	15.6	97.5	31	10	US-09-864-785-2440	Sequence 2440, Ap
405	15.6	97.5	31	10	US-09-864-785-2368	Sequence 2368, Ap	478	15.6	97.5	31	10	US-09-864-785-2441	Sequence 2441, Ap
406	15.6	97.5	31	10	US-09-864-785-2369	Sequence 2369, Ap	479	15.6	97.5	31	10	US-09-864-785-2442	Sequence 2442, Ap
407	15.6	97.5	31	10	US-09-864-785-2370	Sequence 2370, Ap	480	15.6	97.5	31	10	US-09-864-785-2443	Sequence 2443, Ap
408	15.6	97.5	31	10	US-09-864-785-2371	Sequence 2371, Ap	481	15.6	97.5	31	10	US-09-864-785-2444	Sequence 2444, Ap
409	15.6	97.5	31	10	US-09-864-785-2372	Sequence 2372, Ap	482	15.6	97.5	31	10	US-09-864-785-2445	Sequence 2445, Ap
410	15.6	97.5	31	10	US-09-864-785-2373	Sequence 2373, Ap	483	15.6	97.5	31	10	US-09-864-785-2446	Sequence 2446, Ap
411	15.6	97.5	31	10	US-09-864-785-2374	Sequence 2374, Ap	484	15.6	97.5	31	10	US-09-864-785-2447	Sequence 2447, Ap
412	15.6	97.5	31	10	US-09-864-785-2375	Sequence 2375, Ap	485	15.6	97.5	31	10	US-09-864-785-2448	Sequence 2448, Ap
413	15.6	97.5	31	10	US-09-864-785-2376	Sequence 2376, Ap	486	15.6	97.5	31	10	US-09-864-785-2449	Sequence 2449, Ap
414	15.6	97.5	31	10	US-09-864-785-2377	Sequence 2377, Ap	487	15.6	97.5	31	10	US-09-864-785-2450	Sequence 2450, Ap
415	15.6	97.5	31	10	US-09-864-785-2378	Sequence 2378, Ap	488	15.6	97.5	31	10	US-09-864-785-2451	Sequence 2451, Ap
416	15.6	97.5	31	10	US-09-864-785-2379	Sequence 2379, Ap	489	15.6	97.5	31	10	US-09-864-785-2452	Sequence 2452, Ap
417	15.6	97.5	31	10	US-09-864-785-2380	Sequence 2380, Ap	490	15.6	97.5	31	10	US-09-864-785-2453	Sequence 2453, Ap
418	15.6	97.5	31	10	US-09-864-785-2381	Sequence 2381, Ap	491	15.6	97.5	31	10	US-09-864-785-2454	Sequence 2454, Ap
419	15.6	97.5	31	10	US-09-864-785-2382	Sequence 2382, Ap	492	15.6	97.5	31	10	US-09-864-785-2455	Sequence 2455, Ap
420	15.6	97.5	31	10	US-09-864-785-2383	Sequence 2383, Ap	493	15.6	97.5	31	10	US-09-864-785-2456	Sequence 2456, Ap
421	15.6	97.5	31	10	US-09-864-785-2384	Sequence 2384, Ap	494	15.6	97.5	31	10	US-09-864-785-2457	Sequence 2457, Ap
422	15.6	97.5	31	10	US-09-864-785-2385	Sequence 2385, Ap	495	15.6	97.5	31	10	US-09-864-785-2458	Sequence 2458, Ap
423	15.6	97.5	31	10	US-09-864-785-2386	Sequence 2386, Ap	496	15.6	97.5	31	10	US-09-864-785-2459	Sequence 2459, Ap
424	15.6	97.5	31	10	US-09-864-785-2387	Sequence 2387, Ap	497	15.6	97.5	31	10	US-09-864-785-2460	Sequence 2460, Ap
425	15.6	97.5	31	10	US-09-864-785-2388	Sequence 2388, Ap	498	15.6	97.5	31	10	US-09-864-785-2461	Sequence 2461, Ap
426	15.6	97.5	31	10	US-09-864-785-2389	Sequence 2389, Ap	499	15.6	97.5	31	10	US-09-864-785-2462	Sequence 2462, Ap
427	15.6	97.5	31	10	US-09-864-785-2390	Sequence 2390, Ap	500	15.6	97.5	31	10	US-09-864-785-2463	Sequence 2463, Ap
428	15.6	97.5	31	10	US-09-864-785-2391	Sequence 2391, Ap	501	15.6	97.5	31	10	US-09-864-785-2464	Sequence 2464, Ap
429	15.6	97.5	31	10	US-09-864-785-2392	Sequence 2392, Ap	502	15.6	97.5	31	10	US-09-864-785-2465	Sequence 2465, Ap
430	15.6	97.5	31	10	US-09-864-785-2393	Sequence 2393, Ap	503	15.6	97.5	31	10	US-09-864-785-2466	Sequence 2466, Ap
431	15.6	97.5	31	10	US-09-864-785-2394	Sequence 2394, Ap	504	15.6	97.5	31	10	US-09-864-785-2467	Sequence 2467, Ap
432	15.6	97.5	31	10	US-09-864-785-2395	Sequence 2395, Ap	505	15.6	97.5	31	10	US-09-864-785-2468	Sequence 2468, Ap
433	15.6	97.5	31	10	US-09-864-785-2396	Sequence 2396, Ap	506	15.6	97.5	31	10	US-09-864-785-2469	Sequence 2469, Ap
434	15.6	97.5	31	10	US-09-864-785-2397	Sequence 2397, Ap	507	15.6	97.5	31	10	US-09-864-785-2470	Sequence 2470, Ap
435	15.6	97.5	31	10	US-09-864-785-2398	Sequence 2398, Ap	508	15.6	97.5	31	10	US-09-864-785-2471	Sequence 2471, Ap
436	15.6	97.5	31	10	US-09-864-785-2399	Sequence 2399, Ap	509	15.6	97.5	31	10	US-09-864-785-2472	Sequence 2472, Ap
437	15.6	97.5	31	10	US-09-864-785-2400	Sequence 2400, Ap	510	15.6	97.5	31	10	US-09-864-785-2473	Sequence 2473, Ap
438	15.6	97.5	31	10	US-09-864-785-2401	Sequence 2401, Ap	511	15.6	97.5	31	10	US-09-864-785-2474	Sequence 2474, Ap
439	15.6	97.5	31	10	US-09-864-785-2402	Sequence 2402, Ap	512	15.6	97.5	31	10	US-09-864-785-2475	Sequence 2475, Ap
440	15.6	97.5	31	10	US-09-864-785-2403	Sequence 2403, Ap	513	15.6	97.5	31	10	US-09-864-785-2476	Sequence 2476, Ap
441	15.6	97.5	31	10	US-09-864-785-2404	Sequence 2404, Ap	514	15.6	97.5	31	10	US-09-864-785-2477	Sequence 2477, Ap
442	15.6	97.5	31	10	US-09-864-785-2405	Sequence 2405, Ap	515	15.6	97.5	31	10	US-09-864-785-2478	Sequence 2478, Ap
443	15.6	97.5	31	10	US-09-864-785-2406	Sequence 2406, Ap	516	15.6	97.5	31	10	US-09-864-785-2479	Sequence 2479, Ap
444	15.6	97.5	31	10	US-09-864-785-2407	Sequence 2407, Ap	517	15.6	97.5	31	10	US-09-864-785-2480	Sequence 2480, Ap
445	15.6	97.5	31	10	US-09-864-785-2408	Sequence 2408, Ap	518	15.6	97.5	31	10	US-09-864-785-2481	Sequence 2481, Ap
446	15.6	97.5	31	10	US-09-864-785-2409	Sequence 2409, Ap	519	15.6	97.5	31	10	US-09-864-785-2482	Sequence 2482, Ap
447	15.6	97.5	31	10	US-09-864-785-2410	Sequence 2410, Ap	520	15.6	97.5	31	10	US-09-864-785-2483	Sequence 2483, Ap
448	15.6	97.5	31	10	US-09-864-785-2411	Sequence 2411, Ap	521	15.6	97.5	31	10	US-09-864-785-2484	Sequence 2484, Ap
449	15.6	97.5	31	10	US-09-864-785-2412	Sequence 2412, Ap	522	15.6	97.5	31	10	US-09-864-785-2485	Sequence 2485, Ap
450	15.6	97.5	31	10	US-09-864-785-2413	Sequence 2413, Ap	523	15.6	97.5	31	10	US-09-864-785-2486	Sequence 2486, Ap
451	15.6	97.5	31	10	US-09-864-785-2414	Sequence 2414, Ap	524	15.6	97.5	31	10	US-09-864-785-2487	Sequence 2487, Ap
452	15.6	97.5	31	10	US-09-864-785-2415	Sequence 2415, Ap	525	15.6	97.5	31	10	US-09-864-785-2488	Sequence 2488, Ap
453	15.6	97.5	31	10	US-09-864-785-2416	Sequence 2416, Ap	526	15.6	97.5	31	10	US-09-864-785-2489	Sequence 2489, Ap



673	15.6	97.5	31	10	US-09-864-785-2636	Sequence 2636, Ap	746	15.6	97.5	31	11	US-09-730-2898-2952	Sequence 2952, Ap
674	15.6	97.5	31	10	US-09-864-785-2637	Sequence 2637, Ap	747	15.6	97.5	31	11	US-09-730-2898-2953	Sequence 2953, Ap
675	15.6	97.5	31	10	US-09-864-785-2638	Sequence 2638, Ap	748	15.6	97.5	31	11	US-09-730-2898-2954	Sequence 2954, Ap
676	15.6	97.5	31	10	US-09-864-785-2639	Sequence 2639, Ap	749	15.6	97.5	31	11	US-09-730-2898-2955	Sequence 2955, Ap
677	15.6	97.5	31	10	US-09-864-785-2640	Sequence 2640, Ap	750	15.6	97.5	31	11	US-09-730-2898-2956	Sequence 2956, Ap
678	15.6	97.5	31	10	US-09-864-785-2641	Sequence 2641, Ap	751	15.6	97.5	31	11	US-09-730-2898-2957	Sequence 2957, Ap
679	15.6	97.5	31	10	US-09-864-785-2642	Sequence 2642, Ap	752	15.6	97.5	31	11	US-09-730-2898-2958	Sequence 2958, Ap
680	15.6	97.5	31	10	US-09-864-785-2643	Sequence 2643, Ap	753	15.6	97.5	31	11	US-09-730-2898-2959	Sequence 2959, Ap
681	15.6	97.5	31	10	US-09-864-785-2644	Sequence 2644, Ap	754	15.6	97.5	31	11	US-09-730-2898-2960	Sequence 2960, Ap
682	15.6	97.5	31	10	US-09-864-785-2645	Sequence 2645, Ap	755	15.6	97.5	31	11	US-09-730-2898-2961	Sequence 2961, Ap
683	15.6	97.5	31	10	US-09-864-785-2646	Sequence 2646, Ap	756	15.6	97.5	31	11	US-09-730-2898-2962	Sequence 2962, Ap
684	15.6	97.5	31	10	US-09-864-785-2647	Sequence 2647, Ap	757	15.6	97.5	31	11	US-09-730-2898-2963	Sequence 2963, Ap
685	15.6	97.5	31	10	US-09-864-785-2648	Sequence 2648, Ap	758	15.6	97.5	31	11	US-09-730-2898-2964	Sequence 2964, Ap
686	15.6	97.5	31	10	US-09-864-785-2649	Sequence 2649, Ap	759	15.6	97.5	31	11	US-09-730-2898-2965	Sequence 2965, Ap
687	15.6	97.5	31	10	US-09-864-785-2650	Sequence 2650, Ap	760	15.6	97.5	31	11	US-09-730-2898-2966	Sequence 2966, Ap
688	15.6	97.5	31	10	US-09-864-785-2651	Sequence 2651, Ap	761	15.6	97.5	31	11	US-09-730-2898-2967	Sequence 2967, Ap
689	15.6	97.5	31	10	US-09-864-785-2652	Sequence 2652, Ap	762	15.6	97.5	31	11	US-09-730-2898-2968	Sequence 2968, Ap
690	15.6	97.5	31	10	US-09-864-785-2653	Sequence 2653, Ap	763	15.6	97.5	31	11	US-09-730-2898-2969	Sequence 2969, Ap
691	15.6	97.5	31	10	US-09-864-785-2654	Sequence 2654, Ap	764	15.6	97.5	31	11	US-09-730-2898-2970	Sequence 2970, Ap
692	15.6	97.5	31	10	US-09-864-785-2655	Sequence 2655, Ap	765	15.6	97.5	31	11	US-09-730-2898-2971	Sequence 2971, Ap
693	15.6	97.5	31	10	US-09-864-785-2656	Sequence 2656, Ap	766	15.6	97.5	31	11	US-09-730-2898-2972	Sequence 2972, Ap
694	15.6	97.5	31	11	US-09-730-2898-2900	Sequence 2900, Ap	767	15.6	97.5	31	11	US-09-730-2898-2973	Sequence 2973, Ap
695	15.6	97.5	31	11	US-09-730-2898-2901	Sequence 2901, Ap	768	15.6	97.5	31	11	US-09-730-2898-2974	Sequence 2974, Ap
696	15.6	97.5	31	11	US-09-730-2898-2902	Sequence 2902, Ap	769	15.6	97.5	31	11	US-09-730-2898-2975	Sequence 2975, Ap
697	15.6	97.5	31	11	US-09-730-2898-2903	Sequence 2903, Ap	770	15.6	97.5	31	11	US-09-730-2898-2976	Sequence 2976, Ap
698	15.6	97.5	31	11	US-09-730-2898-2904	Sequence 2904, Ap	771	15.6	97.5	31	11	US-09-730-2898-2977	Sequence 2977, Ap
699	15.6	97.5	31	11	US-09-730-2898-2905	Sequence 2905, Ap	772	15.6	97.5	31	11	US-09-730-2898-2978	Sequence 2978, Ap
700	15.6	97.5	31	11	US-09-730-2898-2906	Sequence 2906, Ap	773	15.6	97.5	31	11	US-09-730-2898-2979	Sequence 2979, Ap
701	15.6	97.5	31	11	US-09-730-2898-2907	Sequence 2907, Ap	774	15.6	97.5	31	11	US-09-730-2898-2980	Sequence 2980, Ap
702	15.6	97.5	31	11	US-09-730-2898-2908	Sequence 2908, Ap	775	15.6	97.5	31	11	US-09-730-2898-2981	Sequence 2981, Ap
703	15.6	97.5	31	11	US-09-730-2898-2909	Sequence 2909, Ap	776	15.6	97.5	31	11	US-09-730-2898-2982	Sequence 2982, Ap
704	15.6	97.5	31	11	US-09-730-2898-2910	Sequence 2910, Ap	777	15.6	97.5	31	11	US-09-730-2898-2983	Sequence 2983, Ap
705	15.6	97.5	31	11	US-09-730-2898-2911	Sequence 2911, Ap	778	15.6	97.5	31	11	US-09-730-2898-2984	Sequence 2984, Ap
706	15.6	97.5	31	11	US-09-730-2898-2912	Sequence 2912, Ap	779	15.6	97.5	31	11	US-09-730-2898-2985	Sequence 2985, Ap
707	15.6	97.5	31	11	US-09-730-2898-2913	Sequence 2913, Ap	780	15.6	97.5	31	11	US-09-730-2898-2986	Sequence 2986, Ap
708	15.6	97.5	31	11	US-09-730-2898-2914	Sequence 2914, Ap	781	15.6	97.5	31	11	US-09-730-2898-2987	Sequence 2987, Ap
709	15.6	97.5	31	11	US-09-730-2898-2915	Sequence 2915, Ap	782	15.6	97.5	31	11	US-09-730-2898-2988	Sequence 2988, Ap
710	15.6	97.5	31	11	US-09-730-2898-2916	Sequence 2916, Ap	783	15.6	97.5	31	11	US-09-730-2898-2989	Sequence 2989, Ap
711	15.6	97.5	31	11	US-09-730-2898-2917	Sequence 2917, Ap	784	15.6	97.5	31	11	US-09-730-2898-2990	Sequence 2990, Ap
712	15.6	97.5	31	11	US-09-730-2898-2918	Sequence 2918, Ap	785	15.6	97.5	31	11	US-09-730-2898-2991	Sequence 2991, Ap
713	15.6	97.5	31	11	US-09-730-2898-2919	Sequence 2919, Ap	786	15.6	97.5	31	11	US-09-730-2898-2992	Sequence 2992, Ap
714	15.6	97.5	31	11	US-09-730-2898-2920	Sequence 2920, Ap	787	15.6	97.5	31	11	US-09-730-2898-2993	Sequence 2993, Ap
715	15.6	97.5	31	11	US-09-730-2898-2921	Sequence 2921, Ap	788	15.6	97.5	31	11	US-09-730-2898-2994	Sequence 2994, Ap
716	15.6	97.5	31	11	US-09-730-2898-2922	Sequence 2922, Ap	789	15.6	97.5	31	11	US-09-730-2898-2995	Sequence 2995, Ap
717	15.6	97.5	31	11	US-09-730-2898-2923	Sequence 2923, Ap	790	15.6	97.5	31	11	US-09-730-2898-2996	Sequence 2996, Ap
718	15.6	97.5	31	11	US-09-730-2898-2924	Sequence 2924, Ap	791	15.6	97.5	31	11	US-09-730-2898-2997	Sequence 2997, Ap
719	15.6	97.5	31	11	US-09-730-2898-2925	Sequence 2925, Ap	792	15.6	97.5	31	11	US-09-730-2898-2998	Sequence 2998, Ap
720	15.6	97.5	31	11	US-09-730-2898-2926	Sequence 2926, Ap	793	15.6	97.5	31	11	US-09-730-2898-2999	Sequence 2999, Ap
721	15.6	97.5	31	11	US-09-730-2898-2927	Sequence 2927, Ap	794	15.6	97.5	31	11	US-09-730-2898-3000	Sequence 3000, Ap
722	15.6	97.5	31	11	US-09-730-2898-2928	Sequence 2928, Ap	795	15.6	97.5	31	11	US-09-730-2898-3001	Sequence 3001, Ap
723	15.6	97.5	31	11	US-09-730-2898-2929	Sequence 2929, Ap	796	15.6	97.5	31	11	US-09-730-2898-3002	Sequence 3002, Ap
724	15.6	97.5	31	11	US-09-730-2898-2930	Sequence 2930, Ap	797	15.6	97.5	31	11	US-09-730-2898-3003	Sequence 3003, Ap
725	15.6	97.5	31	11	US-09-730-2898-2931	Sequence 2931, Ap	798	15.6	97.5	31	11	US-09-730-2898-3004	Sequence 3004, Ap
726	15.6	97.5	31	11	US-09-730-2898-2932	Sequence 2932, Ap	799	15.6	97.5	31	11	US-09-730-2898-3005	Sequence 3005, Ap
727	15.6	97.5	31	11	US-09-730-2898-2933	Sequence 2933, Ap	800	15.6	97.5	31	11	US-09-730-2898-3006	Sequence 3006, Ap
728	15.6	97.5	31	11	US-09-730-2898-2934	Sequence 2934, Ap	801	15.6	97.5	31	11	US-09-730-2898-3007	Sequence 3007, Ap
729	15.6	97.5	31	11	US-09-730-2898-2935	Sequence 2935, Ap	802	15.6	97.5	31	11	US-09-730-2898-3008	Sequence 3008, Ap
730	15.6	97.5	31	11	US-09-730-2898-2936	Sequence 2936, Ap	803	15.6	97.5	31	11	US-09-730-2898-3009	Sequence 3009, Ap
731	15.6	97.5	31	11	US-09-730-2898-2937	Sequence 2937, Ap	804	15.6	97.5	31	11	US-09-730-2898-3010	Sequence 3010, Ap
732	15.6	97.5	31	11	US-09-730-2898-2938	Sequence 2938, Ap	805	15.6	97.5	31	11	US-09-730-2898-3011	Sequence 3011, Ap
733	15.6	97.5	31	11	US-09-730-2898-2939	Sequence 2939, Ap	806	15.6	97.5	31	11	US-09-730-2898-3012	Sequence 3012, Ap
734	15.6	97.5	31	11	US-09-730-2898-2940	Sequence 2940, Ap	807	15.6	97.5	31	11	US-09-730-2898-3013	Sequence 3013, Ap
735	15.6	97.5	31	11	US-09-730-2898-2941	Sequence 2941, Ap	808	15.6	97.5	31	11	US-09-730-2898-3014	Sequence 3014, Ap
736	15.6	97.5	31	11	US-09-730-2898-2942	Sequence 2942, Ap	809	15.6	97.5	31	11	US-09-730-2898-3015	Sequence 3015, Ap
737	15.6	97.5	31	11	US-09-730-2898-2943	Sequence 2943, Ap	810	15.6	97.5	31	11	US-09-730-2898-3016	Sequence 3016, Ap
738	15.6	97.5	31	11	US-09-730-2898-2944	Sequence 2944, Ap	811	15.6	97.5	31	11	US-09-730-2898-3017	Sequence 3017, Ap
739	15.6	97.5	31	11	US-09-730-2898-2945	Sequence 2945, Ap	812	15.6	97.5	31	11	US-09-730-2898-3018	Sequence 3018, Ap
740	15.6	97.5	31	11	US-09-730-2898-2946	Sequence 2946, Ap	813	15.6	97.5	31	11	US-09-730-2898-3019	Sequence 3019, Ap
741	15.6	97.5	31	11	US-09-730-2898-2947	Sequence 2947, Ap	814	15.6	97.5	31	11	US-09-730-2898-3020	Sequence 3020, Ap
742	15.6	97.5	31	11	US-09-730-2898-2948	Sequence 2948, Ap	815	15.6	97.5	31	11	US-09-730-2898-3021	Sequence 3021, Ap
743	15.6	97.5	31	11	US-09-730-2898-2949	Sequence 2949, Ap	816	15.6	97.5	31	11	US-09-730-2898-3022	Sequence 3022, Ap
744	15.6	97.5	31	11	US-09-730-2898-2950	Sequence 2950, Ap	817	15.6	97.5	31	11	US-09-730-2898-3023	Sequence 3023, Ap
745	15.6	97.5	31	11	US-09-730-2898-2951	Sequence 2951, Ap	818	15.6	97.5	31	11	US-09-730-2898-3024	Sequence 3024, Ap

819	15.6	97.5	31	11	US-09-730-2898-3025	Sequence 3025, Ap	892	15.6	97.5	31	11	US-09-730-2898-3098	Sequence 3098, Ap
820	15.6	97.5	31	11	US-09-730-2898-3026	Sequence 3026, Ap	893	15.6	97.5	31	11	US-09-730-2898-3099	Sequence 3099, Ap
821	15.6	97.5	31	11	US-09-730-2898-3027	Sequence 3027, Ap	894	15.6	97.5	31	11	US-09-730-2898-3100	Sequence 3100, Ap
822	15.6	97.5	31	11	US-09-730-2898-3028	Sequence 3028, Ap	895	15.6	97.5	31	11	US-09-730-2898-3101	Sequence 3101, Ap
823	15.6	97.5	31	11	US-09-730-2898-3029	Sequence 3029, Ap	896	15.6	97.5	31	11	US-09-730-2898-3102	Sequence 3102, Ap
824	15.6	97.5	31	11	US-09-730-2898-3030	Sequence 3030, Ap	897	15.6	97.5	31	11	US-09-730-2898-3103	Sequence 3103, Ap
825	15.6	97.5	31	11	US-09-730-2898-3031	Sequence 3031, Ap	898	15.6	97.5	31	11	US-09-730-2898-3104	Sequence 3104, Ap
826	15.6	97.5	31	11	US-09-730-2898-3032	Sequence 3032, Ap	899	15.6	97.5	31	11	US-09-730-2898-3105	Sequence 3105, Ap
827	15.6	97.5	31	11	US-09-730-2898-3033	Sequence 3033, Ap	900	15.6	97.5	31	11	US-09-730-2898-3106	Sequence 3106, Ap
828	15.6	97.5	31	11	US-09-730-2898-3034	Sequence 3034, Ap	901	15.6	97.5	31	11	US-09-730-2898-3107	Sequence 3107, Ap
829	15.6	97.5	31	11	US-09-730-2898-3035	Sequence 3035, Ap	902	15.6	97.5	31	11	US-09-730-2898-3108	Sequence 3108, Ap
830	15.6	97.5	31	11	US-09-730-2898-3036	Sequence 3036, Ap	903	15.6	97.5	31	11	US-09-730-2898-3109	Sequence 3109, Ap
831	15.6	97.5	31	11	US-09-730-2898-3037	Sequence 3037, Ap	904	15.6	97.5	31	11	US-09-730-2898-3110	Sequence 3110, Ap
832	15.6	97.5	31	11	US-09-730-2898-3038	Sequence 3038, Ap	905	15.6	97.5	31	11	US-09-730-2898-3111	Sequence 3111, Ap
833	15.6	97.5	31	11	US-09-730-2898-3039	Sequence 3039, Ap	906	15.6	97.5	31	11	US-09-730-2898-3112	Sequence 3112, Ap
834	15.6	97.5	31	11	US-09-730-2898-3040	Sequence 3040, Ap	907	15.6	97.5	31	11	US-09-730-2898-3113	Sequence 3113, Ap
835	15.6	97.5	31	11	US-09-730-2898-3041	Sequence 3041, Ap	908	15.6	97.5	31	11	US-09-730-2898-3114	Sequence 3114, Ap
836	15.6	97.5	31	11	US-09-730-2898-3042	Sequence 3042, Ap	909	15.6	97.5	31	11	US-09-730-2898-3115	Sequence 3115, Ap
837	15.6	97.5	31	11	US-09-730-2898-3043	Sequence 3043, Ap	910	15.6	97.5	31	11	US-09-730-2898-3116	Sequence 3116, Ap
838	15.6	97.5	31	11	US-09-730-2898-3044	Sequence 3044, Ap	911	15.6	97.5	31	11	US-09-730-2898-3117	Sequence 3117, Ap
839	15.6	97.5	31	11	US-09-730-2898-3045	Sequence 3045, Ap	912	15.6	97.5	31	11	US-09-730-2898-3118	Sequence 3118, Ap
840	15.6	97.5	31	11	US-09-730-2898-3046	Sequence 3046, Ap	913	15.6	97.5	31	11	US-09-730-2898-3119	Sequence 3119, Ap
841	15.6	97.5	31	11	US-09-730-2898-3047	Sequence 3047, Ap	914	15.6	97.5	31	11	US-09-730-2898-3120	Sequence 3120, Ap
842	15.6	97.5	31	11	US-09-730-2898-3048	Sequence 3048, Ap	915	15.6	97.5	31	11	US-09-730-2898-3121	Sequence 3121, Ap
843	15.6	97.5	31	11	US-09-730-2898-3049	Sequence 3049, Ap	916	15.6	97.5	31	11	US-09-730-2898-3122	Sequence 3122, Ap
844	15.6	97.5	31	11	US-09-730-2898-3050	Sequence 3050, Ap	917	15.6	97.5	31	11	US-09-730-2898-3123	Sequence 3123, Ap
845	15.6	97.5	31	11	US-09-730-2898-3051	Sequence 3051, Ap	918	15.6	97.5	31	11	US-09-730-2898-3124	Sequence 3124, Ap
846	15.6	97.5	31	11	US-09-730-2898-3052	Sequence 3052, Ap	919	15.6	97.5	31	11	US-09-730-2898-3125	Sequence 3125, Ap
847	15.6	97.5	31	11	US-09-730-2898-3053	Sequence 3053, Ap	920	15.6	97.5	31	11	US-09-730-2898-3126	Sequence 3126, Ap
848	15.6	97.5	31	11	US-09-730-2898-3054	Sequence 3054, Ap	921	15.6	97.5	31	11	US-09-730-2898-3127	Sequence 3127, Ap
849	15.6	97.5	31	11	US-09-730-2898-3055	Sequence 3055, Ap	922	15.6	97.5	31	11	US-09-730-2898-3128	Sequence 3128, Ap
850	15.6	97.5	31	11	US-09-730-2898-3056	Sequence 3056, Ap	923	15.6	97.5	31	11	US-09-730-2898-3129	Sequence 3129, Ap
851	15.6	97.5	31	11	US-09-730-2898-3057	Sequence 3057, Ap	924	15.6	97.5	31	11	US-09-730-2898-3130	Sequence 3130, Ap
852	15.6	97.5	31	11	US-09-730-2898-3058	Sequence 3058, Ap	925	15.6	97.5	31	11	US-09-730-2898-3131	Sequence 3131, Ap
853	15.6	97.5	31	11	US-09-730-2898-3059	Sequence 3059, Ap	926	15.6	97.5	31	11	US-09-730-2898-3132	Sequence 3132, Ap
854	15.6	97.5	31	11	US-09-730-2898-3060	Sequence 3060, Ap	927	15.6	97.5	31	11	US-09-730-2898-3133	Sequence 3133, Ap
855	15.6	97.5	31	11	US-09-730-2898-3061	Sequence 3061, Ap	928	15.6	97.5	31	11	US-09-730-2898-3134	Sequence 3134, Ap
856	15.6	97.5	31	11	US-09-730-2898-3062	Sequence 3062, Ap	929	15.6	97.5	31	11	US-09-730-2898-3135	Sequence 3135, Ap
857	15.6	97.5	31	11	US-09-730-2898-3063	Sequence 3063, Ap	930	15.6	97.5	31	11	US-09-730-2898-3136	Sequence 3136, Ap
858	15.6	97.5	31	11	US-09-730-2898-3064	Sequence 3064, Ap	931	15.6	97.5	31	11	US-09-730-2898-3137	Sequence 3137, Ap
859	15.6	97.5	31	11	US-09-730-2898-3065	Sequence 3065, Ap	932	15.6	97.5	31	11	US-09-730-2898-3138	Sequence 3138, Ap
860	15.6	97.5	31	11	US-09-730-2898-3066	Sequence 3066, Ap	933	15.6	97.5	31	11	US-09-730-2898-3139	Sequence 3139, Ap
861	15.6	97.5	31	11	US-09-730-2898-3067	Sequence 3067, Ap	934	15.6	97.5	31	11	US-09-730-2898-3140	Sequence 3140, Ap
862	15.6	97.5	31	11	US-09-730-2898-3068	Sequence 3068, Ap	935	15.6	97.5	31	11	US-09-730-2898-3141	Sequence 3141, Ap
863	15.6	97.5	31	11	US-09-730-2898-3069	Sequence 3069, Ap	936	15.6	97.5	31	11	US-09-730-2898-3142	Sequence 3142, Ap
864	15.6	97.5	31	11	US-09-730-2898-3070	Sequence 3070, Ap	937	15.6	97.5	31	11	US-09-730-2898-3143	Sequence 3143, Ap
865	15.6	97.5	31	11	US-09-730-2898-3071	Sequence 3071, Ap	938	15.6	97.5	31	11	US-09-730-2898-3144	Sequence 3144, Ap
866	15.6	97.5	31	11	US-09-730-2898-3072	Sequence 3072, Ap	939	15.6	97.5	31	11	US-09-730-2898-3145	Sequence 3145, Ap
867	15.6	97.5	31	11	US-09-730-2898-3073	Sequence 3073, Ap	940	15.6	97.5	31	11	US-09-730-2898-3146	Sequence 3146, Ap
868	15.6	97.5	31	11	US-09-730-2898-3074	Sequence 3074, Ap	941	15.6	97.5	31	11	US-09-730-2898-3147	Sequence 3147, Ap
869	15.6	97.5	31	11	US-09-730-2898-3075	Sequence 3075, Ap	942	15.6	97.5	31	11	US-09-730-2898-3148	Sequence 3148, Ap
870	15.6	97.5	31	11	US-09-730-2898-3076	Sequence 3076, Ap	943	15.6	97.5	31	11	US-09-730-2898-3149	Sequence 3149, Ap
871	15.6	97.5	31	11	US-09-730-2898-3077	Sequence 3077, Ap	944	15.6	97.5	31	11	US-09-730-2898-3150	Sequence 3150, Ap
872	15.6	97.5	31	11	US-09-730-2898-3078	Sequence 3078, Ap	945	15.6	97.5	31	11	US-09-730-2898-3151	Sequence 3151, Ap
873	15.6	97.5	31	11	US-09-730-2898-3079	Sequence 3079, Ap	946	15.6	97.5	31	11	US-09-730-2898-3152	Sequence 3152, Ap
874	15.6	97.5	31	11	US-09-730-2898-3080	Sequence 3080, Ap	947	15.6	97.5	31	11	US-09-730-2898-3153	Sequence 3153, Ap
875	15.6	97.5	31	11	US-09-730-2898-3081	Sequence 3081, Ap	948	15.6	97.5	31	11	US-09-730-2898-3154	Sequence 3154, Ap
876	15.6	97.5	31	11	US-09-730-2898-3082	Sequence 3082, Ap	949	15.6	97.5	31	11	US-09-730-2898-3155	Sequence 3155, Ap
877	15.6	97.5	31	11	US-09-730-2898-3083	Sequence 3083, Ap	950	15.6	97.5	31	11	US-09-730-2898-3156	Sequence 3156, Ap
878	15.6	97.5	31	11	US-09-730-2898-3084	Sequence 3084, Ap	951	15.6	97.5	31	11	US-09-730-2898-3157	Sequence 3157, Ap
879	15.6	97.5	31	11	US-09-730-2898-3085	Sequence 3085, Ap	952	15.6	97.5	31	11	US-09-730-2898-3158	Sequence 3158, Ap
880	15.6	97.5	31	11	US-09-730-2898-3086	Sequence 3086, Ap	953	15.6	97.5	31	11	US-09-730-2898-3159	Sequence 3159, Ap
881	15.6	97.5	31	11	US-09-730-2898-3087	Sequence 3087, Ap	954	15.6	97.5	31	11	US-09-730-2898-3160	Sequence 3160, Ap
882	15.6	97.5	31	11	US-09-730-2898-3088	Sequence 3088, Ap	955	15.6	97.5	31	11	US-09-730-2898-3161	Sequence 3161, Ap
883	15.6	97.5	31	11	US-09-730-2898-3089	Sequence 3089, Ap	956	15.6	97.5	31	11	US-09-730-2898-3162	Sequence 3162, Ap
884	15.6	97.5	31	11	US-09-730-2898-3090	Sequence 3090, Ap	957	15.6	97.5	31	11	US-09-730-2898-3163	Sequence 3163, Ap
885	15.6	97.5	31	11	US-09-730-2898-3091	Sequence 3091, Ap	958	15.6	97.5	31	11	US-09-730-2898-3164	Sequence 3164, Ap
886	15.6	97.5	31	11	US-09-730-2898-3092	Sequence 3092, Ap	959	15.6	97.5	31	11	US-09-730-2898-3165	Sequence 3165, Ap
887	15.6	97.5	31	11	US-09-730-2898-3093	Sequence 3093, Ap	960	15.6	97.5	31	11	US-09-730-2898-3166	Sequence 3166, Ap
888	15.6	97.5	31	11	US-09-730-2898-3094	Sequence 3094, Ap	961	15.6	97.5	31	11	US-09-730-2898-3167	Sequence 3167, Ap
889	15.6	97.5	31	11	US-09-730-2898-3095	Sequence 3095, Ap	962	15.6	97.5	31	11	US-09-730-2898-3168	Sequence 3168, Ap
890	15.6	97.5	31	11	US-09-730-2898-3096	Sequence 3096, Ap	963	15.6	97.5	31	11	US-09-730-2898-3169	Sequence 3169, Ap
891	15.6	97.5	31	11	US-09-730-2898-3097	Sequence 3097, Ap	964	15.6	97.5	31	11	US-09-730-2898-3170	Sequence 3170, Ap

965 15.6 97.5 31 11 US-09-730-289B-3171 Sequence 3171, Ap  
966 15.6 97.5 31 11 US-09-730-289B-3172 Sequence 3172, Ap  
967 15.6 97.5 31 11 US-09-730-289B-3173 Sequence 3173, Ap  
968 15.6 97.5 31 11 US-09-730-289B-3174 Sequence 3174, Ap  
969 15.6 97.5 31 11 US-09-730-289B-3175 Sequence 3175, Ap  
970 15.6 97.5 31 11 US-09-730-289B-3176 Sequence 3176, Ap  
971 15.6 97.5 31 11 US-09-730-289B-3177 Sequence 3177, Ap  
972 15.6 97.5 31 11 US-09-730-289B-3178 Sequence 3178, Ap  
973 15.6 97.5 31 11 US-09-730-289B-3179 Sequence 3179, Ap  
974 15.6 97.5 31 11 US-09-730-289B-3180 Sequence 3180, Ap  
975 15.6 97.5 31 11 US-09-730-289B-3181 Sequence 3181, Ap  
976 15.6 97.5 31 11 US-09-730-289B-3182 Sequence 3182, Ap  
977 15.6 97.5 31 11 US-09-730-289B-3183 Sequence 3183, Ap  
978 15.6 97.5 31 11 US-09-730-289B-3184 Sequence 3184, Ap  
979 15.6 97.5 31 11 US-09-730-289B-3185 Sequence 3185, Ap  
980 15.6 97.5 31 11 US-09-730-289B-3186 Sequence 3186, Ap  
981 15.6 97.5 31 11 US-09-730-289B-3187 Sequence 3187, Ap  
982 15.6 97.5 31 11 US-09-730-289B-3188 Sequence 3188, Ap  
983 15.6 97.5 31 11 US-09-730-289B-3189 Sequence 3189, Ap  
984 15.6 97.5 31 11 US-09-730-289B-3190 Sequence 3190, Ap  
985 15.6 97.5 31 11 US-09-730-289B-3191 Sequence 3191, Ap  
986 15.6 97.5 31 11 US-09-730-289B-3192 Sequence 3192, Ap  
987 15.6 97.5 31 11 US-09-730-289B-3193 Sequence 3193, Ap  
988 15.6 97.5 31 11 US-09-730-289B-3194 Sequence 3194, Ap  
989 15.6 97.5 31 11 US-09-730-289B-3195 Sequence 3195, Ap  
990 15.6 97.5 31 11 US-09-730-289B-3196 Sequence 3196, Ap  
991 15.6 97.5 31 11 US-09-730-289B-3197 Sequence 3197, Ap  
992 15.6 97.5 31 11 US-09-730-289B-3198 Sequence 3198, Ap  
993 15.6 97.5 31 11 US-09-730-289B-3199 Sequence 3199, Ap  
994 15.6 97.5 31 11 US-09-730-289B-3200 Sequence 3200, Ap  
995 15.6 97.5 31 11 US-09-730-289B-3201 Sequence 3201, Ap  
996 15.6 97.5 31 11 US-09-730-289B-3202 Sequence 3202, Ap  
997 15.6 97.5 31 11 US-09-730-289B-3203 Sequence 3203, Ap  
998 15.6 97.5 31 11 US-09-730-289B-3204 Sequence 3204, Ap  
999 15.6 97.5 31 11 US-09-730-289B-3205 Sequence 3205, Ap  
1000 15.6 97.5 31 11 US-09-730-289B-3206 Sequence 3206, Ap

## ALIGNMENTS

RESULT 1  
US-09-877-526A-21  
Sequence 21, Application US/09877526A  
Patent No. US20020102568A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc  
APPLICANT: Uman, Nassim  
APPLICANT: McSwigen, Jim  
APPLICANT: Zinnen, Shawn  
APPLICANT: Seiwert, Scott  
APPLICANT: Haebertl, Pete  
APPLICANT: Chowritza, Bharat  
APPLICANT: Blact, Larry  
APPLICANT: Valish, Narendra  
TITLE OF INVENTION: A Process for the Detection of Nucleic Acid Using Nucleic Acid Ca  
FILE REFERENCE: MBH00-816-C (700/002)  
CURRENT APPLICATION NUMBER: US/09/877, 526A  
CURRENT FILING DATE: 2001-03-06  
PRIOR APPLICATION NUMBER: 60/187, 128  
PRIOR FILING DATE: 2000-03-06  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: Patent version 3.0  
SEQ ID NO 21  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif  
US-09-877-526A-21

Query Match 97.5%, Score 15.6, DB 10, Length 16;  
Best Local Similarity 100.0%, Pred. No. 23;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 2  
US-09-866-316B-15  
Sequence 15, Application US/09866316B  
Patent No. US20020142980A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Thompson, Jim  
APPLICANT: McSwigen, Jim  
APPLICANT: Haebertl, Pete  
APPLICANT: Beigelman, Leo  
APPLICANT: Karpelesky, Alex  
APPLICANT: Bellon, Lauren  
APPLICANT: Reynolds, Mark  
APPLICANT: Zwack, Michael  
APPLICANT: Jarvis, Thale  
APPLICANT: Woolf, Todd  
APPLICANT: Maculic-Adamic, Jasenka  
TITLE OF INVENTION: Nucleic Acid Molecules with No. US20020142980A1 Chemical Compos  
FILE REFERENCE: MBH00, 873-H 500/004  
CURRENT APPLICATION NUMBER: US/09/866, 316B  
CURRENT FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 09/103, 656  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: US 60/082, 404  
PRIOR FILING DATE: 1998-04-20  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent version 3.0  
SEQ ID NO 15  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNzyme Motif  
US-09-866-316B-15

Query Match 97.5%, Score 15.6, DB 10, Length 16;  
Best Local Similarity 100.0%, Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 3  
US-09-864-785-3928  
Sequence 3928, Application US/09864785  
Patent No. US20020175568A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Draper, Ken  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
FILE REFERENCE: 400/022 (MBH00-812-D)  
CURRENT APPLICATION NUMBER: US/09/864, 785  
CURRENT FILING DATE: 2001-05-23  
NUMBER OF SEQ ID NOS: 3928  
SOFTWARE: Patent version 3.0  
SEQ ID NO 3928  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-3928

Query Match 97.5%; Score 15.6; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
|||||  
DB 1 RGCTAGCTACACGA 16

RESULT 4  
US-09-992-160-21  
Sequence 21, Application US/09992160  
Publication No. US2003008295A1

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc  
APPLICANT: Uman, Nassim  
APPLICANT: McSwigen, Jim  
APPLICANT: Zinnen, Shawn  
APPLICANT: Seiwert, Scott  
APPLICANT: Haebertl, Pete  
APPLICANT: Chowrira, Bharat  
APPLICANT: Blatt, Larry  
TITLE OF INVENTION: Nucleic Acid Sensor Molecules  
FILE REFERENCE: MBH00-816-D (700/004)  
CURRENT FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 21  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif  
US-09-992-160-21

Query Match 97.5%; Score 15.6; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
|||||  
DB 1 RGCTAGCTACACGA 16

RESULT 5  
US-09-730-289B-3896  
Sequence 3896, Application US/09730289B  
Publication No. US20030050259A1

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
FILE REFERENCE: MBH00-864-A (400/006)  
CURRENT FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: US 60/169,100  
PRIOR FILING DATE: 1999-12-06  
NUMBER OF SEQ ID NOS: 3897  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 3896  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence  
US-09-730-289B-3896

Query Match 97.5%; Score 15.6; DB 11; Length 16;

Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
|||||  
DB 1 RGCTAGCTACACGA 16

RESULT 6  
US-09-780-533A-6679  
Sequence 6679, Application US/09780533A  
Publication No. US2003006011A1

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
APPLICANT: Chowrira, Bharat  
APPLICANT: Haebertl, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
FILE REFERENCE: MBH00-878-A (400/011)  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US/09/780,533A  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 6679  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-533A-6679

Query Match 97.5%; Score 15.6; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16  
|||||  
DB 1 RGCTAGCTACACGA 16

RESULT 7  
US-09-877-478-6585  
Sequence 6585, Application US/09877478  
Publication No. US20030068301A1

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Dreier, Kenneth  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
FILE REFERENCE: MBH00-845-H (400/029)  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: US/09/877,478  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: US 07/882,712  
PRIOR FILING DATE: 1992-05-14  
PRIOR APPLICATION NUMBER: US 09/531,025  
PRIOR FILING DATE: 2000-03-20  
PRIOR APPLICATION NUMBER: US 09/636,385  
PRIOR FILING DATE: 2000-08-09  
PRIOR APPLICATION NUMBER: US 09/696,347  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 08/193,627  
PRIOR FILING DATE: 1994-02-07  
PRIOR APPLICATION NUMBER: US 08/433,993  
PRIOR FILING DATE: 1995-05-04  
PRIOR APPLICATION NUMBER: US 08/434,504  
PRIOR FILING DATE: 1995-05-04  
PRIOR APPLICATION NUMBER: US 09/436,430  
PRIOR FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 6586  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 6585  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-877-478-6585

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
DB 1 RGGCTAGCTACACGA 16

RESULT 8  
US-09-848-754A-9645  
Sequence 9645, Application US/09848754A  
Publication No. US20030073207A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
FILE REFERENCE: MBH00-958-1 (400/018)  
CURRENT APPLICATION NUMBER: US/09/848,754A  
CURRENT FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 9645  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 9645  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme Motif  
US-09-848-754A-9645

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
DB 1 RGGCTAGCTACACGA 16

RESULT 9  
US-09-776-474-2991  
Sequence 2991, Application US/09776474  
Publication No. US20030087847A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Jarvis, Thale  
APPLICANT: Boober, Robert  
APPLICANT: Holman, Patricia  
APPLICANT: Fatmeh, Ali  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK  
FILE REFERENCE: MBH00-955-A (400/008)  
CURRENT APPLICATION NUMBER: US/09/776,474  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: US 60/179,983  
PRIOR FILING DATE: 2000-03-02  
NUMBER OF SEQ ID NOS: 2992  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 2991  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-2991

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
DB 1 RGGCTAGCTACACGA 16

RESULT 10  
US-09-930-423-4549  
Sequence 4549, Application US/09930423  
Publication No. US20030092003A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
FILE REFERENCE: MBH00,918-A 400/027  
CURRENT APPLICATION NUMBER: US/09/930,423  
CURRENT FILING DATE: 2001-08-15  
NUMBER OF SEQ ID NOS: 4553  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 4549  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-930-423-4549

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16  
DB 1 RGGCTAGCTACACGA 16

RESULT 11  
US-09-780-164-2602  
Sequence 2602, Application US/09780164  
Publication No. US20030092646A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20  
FILE REFERENCE: 400/010  
CURRENT APPLICATION NUMBER: US/09/780,164  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/185,516  
PRIOR FILING DATE: 2000-02-28  
NUMBER OF SEQ ID NOS: 2603  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 2602  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-164-2602

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16

Db 1 RGGCTAGCTACACGA 16

RESULT 12  
US-09-827-395A-2617  
; Sequence 2617, Application US/09827395A  
; Publication No. US20030113891A1  
; GENERAL INFORMATION: Pharmaceutical, Inc.  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Lawrence Blatt  
; APPLICANT: James McSwiggan  
; APPLICANT: Bharat Chowitra  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor C  
; FILE REFERENCE: MEH80-878-C (400/017)  
; CURRENT APPLICATION NUMBER: US/09/827,395A  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/780,533  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 2617  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2617  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Definition of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-827-395A-2617

Query Match 97.5%; Score 15.6; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 13  
US-10-366-191-14  
; Sequence 14, Application US/10366191  
; Publication No. US20030228590A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Suban, Radka  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Haebertli, Peter  
; TITLE OF INVENTION: Anticodons Having Specificity for Nucleic Acids  
; FILE REFERENCE: 02-030-A (900/047)  
; CURRENT APPLICATION NUMBER: US/10/366,191  
; CURRENT FILING DATE: 2003-02-12  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-366-191-14

Query Match 97.5%; Score 15.6; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 14

US-10-435-044A-19  
; Sequence 19, Application US/10435044A  
; Publication No. US20030228615A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossi, John J  
; APPLICANT: Scherr, Michaela  
; APPLICANT: Riggs, Arthur D  
; TITLE OF INVENTION: Method For Identifying Accessible Binding Sites on RNA  
; FILE REFERENCE: 1954-2851  
; CURRENT APPLICATION NUMBER: US/10/435,044A  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: US 09/536,393  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/127,529  
; PRIOR FILING DATE: 1999-04-02  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: catalytic core  
US-10-435-044A-19

Query Match 97.5%; Score 15.6; DB 12; Length 16;  
Best Local Similarity 93.8%; Pred. No. 23;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCTACACGA 16  
Db 1 AGGCTAGCTACACGA 16

RESULT 15  
US-10-435-044A-20  
; Sequence 20, Application US/10435044A  
; Publication No. US20030228615A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossi, John J  
; APPLICANT: Scherr, Michaela  
; APPLICANT: Riggs, Arthur D  
; TITLE OF INVENTION: Method For Identifying Accessible Binding Sites on RNA  
; FILE REFERENCE: 1954-2851  
; CURRENT APPLICATION NUMBER: US/10/435,044A  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: US 09/536,393  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/127,529  
; PRIOR FILING DATE: 1999-04-02  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: catalytic core  
US-10-435-044A-20

Query Match 97.5%; Score 15.6; DB 12; Length 16;  
Best Local Similarity 93.8%; Pred. No. 23;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCTACACGA 16  
Db 1 GGGCTAGCTACACGA 16

RESULT 16  
US-09-745-237A-4549  
; Sequence 4549, Application US/09745237A  
; Publication No. US20030143708A1

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwiggen, Jim  
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
FILE REFERENCE: 400/007 (MBH00-918-A)  
CURRENT APPLICATION NUMBER: US/09/745,237A  
CURRENT FILING DATE: 2002-04-15  
NUMBER OF SEQ ID NOS: 4550  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 4549  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence  
US-09-745-237A-4549

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 13; Length 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16  
DB 1 RGGCTAGCTACAACGA 16

RESULT 17  
US-09-792-818-2304  
Sequence 2304, Application US/09792818  
Publication No. US20030134806A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Jarvis, Thale  
APPLICANT: Von Carlowitz, Ira  
APPLICANT: McSwiggen, Jim  
APPLICANT: Hamblin, Paul  
APPLICANT: Ellis, Jonathan  
TITLE OF INVENTION: Method and Reagent for the Inhibition of Gdb-2-related with Inset  
FILE REFERENCE: MBH00-901-A (400/013)  
CURRENT APPLICATION NUMBER: US/09/792,818  
CURRENT FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 2304  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 2304  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-792-818-2304

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 13; Length 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16  
DB 1 RGGCTAGCTACAACGA 16

RESULT 18  
US-10-279-401-11  
Sequence 11, Application US/10279401  
Publication No. US20030149362A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
APPLICANT: Macejak, Dennis  
APPLICANT: Lee, Patrice  
TITLE OF INVENTION: In Vivo Models For Screening Inhibitors of Hepatitis B Virus  
FILE REFERENCE: 400/066 (MBH01-1336-B)  
CURRENT APPLICATION NUMBER: US/10/279,401

CURRENT FILING DATE: 2003-01-27  
PRIOR APPLICATION NUMBER: US 60/296,876  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/335,059  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: PCT/US02/09187  
PRIOR FILING DATE: 2002-03-26  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 11  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNazyme Motif  
US-10-279-401-11

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 13; Length 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16  
DB 1 RGGCTAGCTACAACGA 16

RESULT 19  
US-10-201-389A-13  
Sequence 13, Application US/10201389A  
Publication No. US20030148929A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Beigelman, Leonard  
APPLICANT: Azharyev, Alex  
APPLICANT: Antopolosky, Maxim  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID PEPTIDE CONJUGATES  
FILE REFERENCE: 600/023  
CURRENT APPLICATION NUMBER: US/10/201,389A  
CURRENT FILING DATE: 2002-07-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 13  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNazyme motif  
US-10-201-389A-13

Query Match  
Best Local Similarity 97.5%; Score 15.6; DB 13; Length 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16  
DB 1 RGGCTAGCTACAACGA 16

RESULT 20  
US-10-238-700-4666  
Sequence 4666, Application US/10238700  
Publication No. US20030153521A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
FILE REFERENCE: 400/057 (MBH01-1158-A)  
CURRENT APPLICATION NUMBER: US/10/238,700  
CURRENT FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: PCT/US 02/16840  
PRIOR FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: US 60/318,471

PRIOR FILING DATE: 2001-09-10  
NUMBER OF SEQ ID NOS: 4666  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4666  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-238-700-4666

Query Match 97.5%; Score 15.6; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 21  
US-10-277-494-445  
Sequence 445, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwiggen, Jim  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MBH00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 445  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Loop Nucleic Acid Sequence  
US-10-277-494-445

Query Match 97.5%; Score 15.6; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 22  
US-10-230-006-2677  
Sequence 2677, Application US/10230006  
Publication No. US20030191077A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwiggen, Jim  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI  
FILE REFERENCE: 400/056 (MBH00-1110)  
CURRENT APPLICATION NUMBER: US/10/230,006  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: US 60/315,315  
PRIOR FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 2678  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2677  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-10-230-006-2677

Query Match 97.5%; Score 15.6; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 23  
US-10-306-747A-11  
Sequence 11, Application US/10306747A  
Publication No. US20030216335A1  
GENERAL INFORMATION:  
APPLICANT: Sirta Therapeutics, Inc.  
APPLICANT: Sandberg, Jennifer  
APPLICANT: Pavco, Pam  
APPLICANT: Gordon, Glad M.D.  
TITLE OF INVENTION: Method and Reagent for the Modulation of Female Reproductive Dis  
FILE REFERENCE: 01-1735-A (400/070)  
CURRENT APPLICATION NUMBER: US/10/306,747A  
CURRENT FILING DATE: 2002-11-27  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-306-747A-11

Query Match 97.5%; Score 15.6; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 1 RGGCTAGCTACACGA 16

RESULT 24  
US-10-151-116-12  
Sequence 12, Application US/10151116  
Publication No. US20030104985A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Matulic-Adamic, Jasenka  
APPLICANT: Beigelman, Leo  
TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery  
FILE REFERENCE: MBH 01,639-B (600/020)  
CURRENT APPLICATION NUMBER: US/10/151,116  
CURRENT FILING DATE: 2002-05-17  
PRIOR APPLICATION NUMBER: 60/362,016  
PRIOR FILING DATE: 2002-03-06  
PRIOR APPLICATION NUMBER: 60/292,217  
PRIOR FILING DATE: 2001-05-18  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 12  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme motif  
US-10-151-116-12

Query Match 97.5%; Score 15.6; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
| | | | | | | | | |  
DB 1 RGCTAGCTACACGA 16

## RESULT 25

US-10-163-552-1997  
; Sequence 1997, Application US/10163552  
; Publication No. US20030105051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level  
; TITLE OF INVENTION: HER2  
; FILE REFERENCE: MHB01-1653-A (400/014)  
; CURRENT APPLICATION NUMBER: US/10/163,552  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 1997  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 1997  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Substrate Sequence  
US-10-163-552-1997

Query Match 97.5%; Score 15.6; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
| | | | | | | | | |  
DB 1 RGCTAGCTACACGA 16

## RESULT 26

US-10-156-306-8013  
; Sequence 8013, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 8013  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Substrate sequence  
US-10-156-306-8013

Query Match 97.5%; Score 15.6; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
| | | | | | | | | |  
DB 1 RGCTAGCTACACGA 16

RESULT 27  
US-10-157-580A-170  
; Sequence 170, Application US/10157580A  
; Publication No. US20030124513A1  
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related To Levels of HIV  
; FILE REFERENCE: MHB01-665-A (400/051)  
; CURRENT APPLICATION NUMBER: US/10/157,580A  
; CURRENT FILING DATE: 2002-08-30  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 170  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif  
US-10-157-580A-170

Query Match 97.5%; Score 15.6; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
| | | | | | | | | |  
DB 1 RGCTAGCTACACGA 16

## RESULT 28

US-10-201-394A-13  
; Sequence 13, Application US/10201394A  
; Publication No. US20030130186A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Vargese, Chandra  
; APPLICANT: Adamic, Jasenka  
; APPLICANT: Karpeisky, Alexander  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: CONJUGATES AND COMPOSITIONS FOR CELLULAR DELIVERY  
; FILE REFERENCE: MHB01-882-B (600/022)  
; CURRENT APPLICATION NUMBER: US/10/201,394A  
; CURRENT FILING DATE: 2002-07-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 13  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-201-394A-13

Query Match 97.5%; Score 15.6; DB 16; Length 16;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
| | | | | | | | | |  
DB 1 RGCTAGCTACACGA 16

## RESULT 29

US-10-277-494-334  
; Sequence 334, Application US/10277494  
; Publication No. US20030186909A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level  
; TITLE OF INVENTION: Epidermal Growth Factor Receptors  
; FILE REFERENCE: MHB00-958-K (400/064)  
; CURRENT APPLICATION NUMBER: US/10/277,494  
; CURRENT FILING DATE: 2002-10-21  
; NUMBER OF SEQ ID NOS: 446

SOFTWARE: Patentin version 3.0  
SEQ ID NO 334  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-334

Query Match 97.5%; Score 15.6; DB 13; Length 23;  
Best Local Similarity 93.8%; Pred. No. 23;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 4 GGGCTAGCTACACGA 19

RESULT 30  
US-10-277-494-335  
Sequence 335, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: McSwigen, Jim  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MHB00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 335  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-335

Query Match 97.5%; Score 15.6; DB 13; Length 23;  
Best Local Similarity 93.8%; Pred. No. 23;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 4 GGGCTAGCTACACGA 19

RESULT 31  
US-10-277-494-336  
Sequence 336, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: McSwigen, Jim  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MHB00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 336  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-336

Query Match 97.5%; Score 15.6; DB 13; Length 23;  
Best Local Similarity 93.8%; Pred. No. 23;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGGCTAGCTACACGA 16  
Db 4 GGGCTAGCTACACGA 19

RESULT 32  
US-10-277-494-337  
Sequence 337, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: McSwigen, Jim  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MHB00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 337  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-337

Query Match 97.5%; Score 15.6; DB 13; Length 23;  
Best Local Similarity 93.8%; Pred. No. 23;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 4 GGGCTAGCTACACGA 19

RESULT 33  
US-10-277-494-338  
Sequence 338, Application US/10277494  
Publication No. US20030186909A1  
GENERAL INFORMATION:  
APPLICANT: McSwigen, Jim  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
FILE REFERENCE: MHB00-958-K (400/064)  
CURRENT APPLICATION NUMBER: US/10/277,494  
CURRENT FILING DATE: 2002-10-21  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 338  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
US-10-277-494-338

Query Match 97.5%; Score 15.6; DB 13; Length 23;  
Best Local Similarity 93.8%; Pred. No. 23;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16  
Db 4 GGGCTAGCTACACGA 19

RESULT 34  
US-10-277-494-339  
Sequence 339, Application US/10277494  
Publication No. US20030186909A1

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; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; TITLE OF INVENTION: Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 339
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-339

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
    :|||||
DB 4 GGGCTAGCTACACGA 19

RESULT 35
US-10-277-494-340
; Sequence 340, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; TITLE OF INVENTION: Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 340
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-340

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
    :|||||
DB 4 AGGCTAGCTACACGA 19

RESULT 36
US-10-277-494-341
; Sequence 341, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; TITLE OF INVENTION: Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 341

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```

; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-341

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
    :|||||
DB 4 AGGCTAGCTACACGA 19

RESULT 37
US-10-277-494-342
; Sequence 342, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; TITLE OF INVENTION: Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 342
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-342

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
    :|||||
DB 4 GGGCTAGCTACACGA 19

RESULT 38
US-10-277-494-343
; Sequence 343, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; TITLE OF INVENTION: Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 343
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-343

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Wed Jan 21 10:43:28 2004

OY 1 RGCTAGCTACACGA 16  
 :|||||||  
 Db 4 GGCTAGCTACACGA 19

## RESULT 39

US-10-277-494-344  
 ; Sequence 344, Application US/10277494  
 ; Publication No. US20030186909A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
 ; TITLE OF INVENTION: Epidermal Growth Factor Receptors  
 ; FILE REFERENCE: MBHB00-958-K (400/064)  
 ; CURRENT APPLICATION NUMBER: US/10/277,494  
 ; CURRENT FILING DATE: 2002-10-21  
 ; NUMBER OF SEQ ID NOS: 446  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 344  
 ; LENGTH: 23  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
 US-10-277-494-344

Query Match 97.5%; Score 15.6; DB 13; Length 23;  
 Best Local Similarity 93.8%; Pred. No. 23;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
 :|||||||  
 Db 4 AGCTAGCTACACGA 19

## RESULT 40

US-10-277-494-345  
 ; Sequence 345, Application US/10277494  
 ; Publication No. US20030186909A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level  
 ; TITLE OF INVENTION: Epidermal Growth Factor Receptors  
 ; FILE REFERENCE: MBHB00-958-K (400/064)  
 ; CURRENT APPLICATION NUMBER: US/10/277,494  
 ; CURRENT FILING DATE: 2002-10-21  
 ; NUMBER OF SEQ ID NOS: 446  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 345  
 ; LENGTH: 23  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec  
 US-10-277-494-345

Query Match 97.5%; Score 15.6; DB 13; Length 23;  
 Best Local Similarity 93.8%; Pred. No. 23;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16  
 :|||||||  
 Db 4 GGCTAGCTACACGA 19

Search completed: January 21, 2004, 08:22:20  
 Job time : 157 secs

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